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(54) Title: 28 HUMAN SECRETED PROTEINS			
(57) Abstract			
<p>The present invention relates to 28 human secreted proteins and isolated nucleic acids containing the coding regions of the genes encoding such proteins. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating disorders related to these novel human secreted proteins.</p>			

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## 28 Human Secreted Proteins

### *Field of the Invention*

This invention relates to newly identified polynucleotides and the polypeptides encoded by these polynucleotides, uses of such polynucleotides and polypeptides, and their production.

**Background of the Invention**

Unlike bacterium, which exist as a single compartment surrounded by a membrane, human cells and other eucaryotes are subdivided by membranes into many functionally distinct compartments. Each membrane-bounded compartment, or 10 organelle, contains different proteins essential for the function of the organelle. The cell uses "sorting signals," which are amino acid motifs located within the protein, to target proteins to particular cellular organelles.

One type of sorting signal, called a signal sequence, a signal peptide, or a leader sequence, directs a class of proteins to an organelle called the endoplasmic reticulum 15 (ER). The ER separates the membrane-bounded proteins from all other types of proteins. Once localized to the ER, both groups of proteins can be further directed to another organelle called the Golgi apparatus. Here, the Golgi distributes the proteins to vesicles, including secretory vesicles, the cell membrane, lysosomes, and the other organelles.

20 Proteins targeted to the ER by a signal sequence can be released into the extracellular space as a secreted protein. For example, vesicles containing secreted proteins can fuse with the cell membrane and release their contents into the extracellular space - a process called exocytosis. Exocytosis can occur constitutively or after receipt of a triggering signal. In the latter case, the proteins are stored in secretory vesicles (or 25 secretory granules) until exocytosis is triggered. Similarly, proteins residing on the cell membrane can also be secreted into the extracellular space by proteolytic cleavage of a "linker" holding the protein to the membrane.

Despite the great progress made in recent years, only a small number of genes 30 encoding human secreted proteins have been identified. These secreted proteins include the commercially valuable human insulin, interferon, Factor VIII, human growth hormone, tissue plasminogen activator, and erythropoietin. Thus, in light of the pervasive role of secreted proteins in human physiology, a need exists for identifying 35 and characterizing novel human secreted proteins and the genes that encode them. This knowledge will allow one to detect, to treat, and to prevent medical disorders by using secreted proteins or the genes that encode them.

### *Summary of the Invention*

The present invention relates to novel polynucleotides and the encoded polypeptides. Moreover, the present invention relates to vectors, host cells, antibodies, 5 and recombinant methods for producing the polypeptides and polynucleotides. Also provided are diagnostic methods for detecting disorders related to the polypeptides, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying binding partners of the polypeptides.

### 10 *Detailed Description*

#### Definitions

The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

- In the present invention, "isolated" refers to material removed from its original 15 environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide.
- 20 In the present invention, a "secreted" protein refers to those proteins capable of being directed to the ER, secretory vesicles, or the extracellular space as a result of a signal sequence, as well as those proteins released into the extracellular space without necessarily containing a signal sequence. If the secreted protein is released into the extracellular space, the secreted protein can undergo extracellular processing to produce 25 a "mature" protein. Release into the extracellular space can occur by many mechanisms, including exocytosis and proteolytic cleavage.

As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence contained in SEQ ID NO:X or the cDNA contained within the clone deposited with the ATCC. For example, the polynucleotide can contain the nucleotide sequence 30 of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, with or without the signal sequence, the secreted protein coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having the translated amino acid sequence generated from the polynucleotide as broadly defined.

35 In the present invention, the full length sequence identified as SEQ ID NO:X was often generated by overlapping sequences contained in multiple clones (contig

analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X was deposited with the American Type Culture Collection ("ATCC"). As shown in Table 1, each clone is identified by a cDNA Clone ID (Identifier) and the ATCC Deposit Number. The ATCC is located at 12301 Park Lawn Drive, Rockville, Maryland 20852, USA. The ATCC deposit was made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for purposes of patent procedure.

A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained in SEQ ID NO:X, the complement thereof, or the cDNA within the clone deposited with the ATCC. "Stringent hybridization conditions" refers to an overnight incubation at 42°C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM sodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65°C.

Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH<sub>2</sub>PO<sub>4</sub>; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 µg/ml salmon sperm blocking DNA; followed by washes at 50°C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

Of course, a polynucleotide which hybridizes only to polyA+ sequences (such as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a

complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone).

5       The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and  
10      regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability  
15      or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

20      The polypeptide of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs,  
25      as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be  
30      branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a  
35      nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine,

formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins  
5 such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth Enzymol 182:626-646 (1990);  
10 Rattan et al., Ann NY Acad Sci 663:48-62 (1992).)

"SEQ ID NO:X" refers to a polynucleotide sequence while "SEQ ID NO:Y" refers to a polypeptide sequence, both sequences identified by an integer specified in Table 1.

"A polypeptide having biological activity" refers to polypeptides exhibiting 15 activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present  
20 invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention.).

25 **Polynucleotides and Polypeptides of the Invention**

**FEATURES OF PROTEIN ENCODED BY GENE NO: 1**

It has been discovered that this gene is expressed primarily in pituitary and to a lesser extent in T cells and endometrial stromal cells.

Therefore, polynucleotides and polypeptides of the invention are useful as  
30 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, endocrine disorders and inflammation particularly in CNS injury. Similarly, polypeptides and antibodies directed to these polypeptides are in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a  
35 number of disorders of the above tissues or cells, particularly of the immune system and central nervous system, expression of this gene at significantly higher or lower

- levels may be routinely detected in certain tissues and cell types (e.g., pituitary, T-cells, and endometrium, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,
- 5 the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for treating diseases of the endocrine system or disease that result in inflammation in the CNS. This gene maps to chromosome 1 and, therefore, is useful in chromosome  
10 mapping.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 2

The translation product of this gene shares sequence homology with CDC2 serine threonine kinase which is thought to be important in regulating progression  
15 through the cell cycle.

This gene is expressed primarily in adrenal gland tumors and to a lesser extent in brain, pineal gland and gall bladder.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a  
20 biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancers, particularly of the adrenal gland, and endocrine disorders. Similarly, polypeptides and antibodies directed to these polypeptides are in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the adrenal gland,  
25 brain and gall bladder. expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., adrenal gland, brain and other tissue of the nervous system, pineal gland, and gall bladder, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to  
30 the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to CDC2 kinase indicates that the protein product of this clone is useful for treating cancers.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 3**

The translation product of this gene shares sequence homology with egg specific protein of *xenopus* oocytes which may play a role in binding intracellular DNA. See, Genbank accession NO: gil214636 and Eur. J. Biochem. 1992 Jun 15; 206(3):

- 5 673-683. Based on the sequence similarity between the translation product of this gene and egg-specific protein, the translation product of this gene is expected to share certain biological activities with egg-specific protein.

This gene is expressed primarily in placenta and to a lesser extent in T-cells.

- Therefore, polynucleotides and polypeptides of the invention are useful as  
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,  
15 particularly of the immune, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, and T-cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the  
20 expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:53 as residues: Pro-32 to Gly-38.

- The tissue distribution and homology to egg specific protein of *xenopus* oocytes indicates that polynucleotides and polypeptides corresponding to the gene are useful for  
25 treating inflammation mediated by T-cells.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 4**

- The translation product of this gene shares sequence homology with mouse FGD-1 which is thought to be important in regulating the signal transduction response  
30 to small G proteins. See, for example, Genbank accession NO: gil722343.

This gene is expressed primarily in breast lymph nodes, and to a lesser extent in thymus.

- Therefore, polynucleotides and polypeptides of the invention are useful as  
reagents for differential identification of the tissue(s) or cell type(s) present in a  
35 biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune response particularly in breast cancer. Similarly, polypeptides

- and antibodies directed to these polypeptides are in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.,
- 5        mammary tissue, lymphoid tissue, and thymus, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.
- 10      The tissue distribution and homology to FGD1 indicates that polynucleotides and polypeptides corresponding to the gene are useful for regulating signalling and growth of breast tumors and in inflammatory responses in the immune system.
- FEATURES OF PROTEIN ENCODED BY GENE NO: 5**
- 15      The translation product of this gene shares sequence homology with a gene up-regulated by thyroid hormone in tadpoles and is expressed specifically in the tail and only at metamorphosis. (See Genbank accession NO: 1234787, see also, Brown, D.D., et al., Proc. Natl. Acad. Sci. U.S.A. 93:1924-1929 (1996). This protein is thought to be important in the tail resorption program of *Xenopus laevis*. Preferred
- 20      polypeptide fragments comprise the amino acid sequence: FSVTNNTECGKLLEEEIKC  
ALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCRGHIPGFLQTTADEF  
CFYYARKDGGLCFPDFPRKQVRGPASNYLDQMEEYDKVEEISRKHKNCFCIQ  
EVVSGLRQPVGALHSGDGSQRFILEKEGYVKILTPEGEIFKEPYLDIHKLV  
(SEQ ID NO: 91).
- 25      Also preferred are polynucleotide fragments encoding these polypeptide fragments.
- This gene is expressed primarily in umbilical vein endothelial cells and to a lesser extent primary dendritic cells.
- Therefore, polynucleotides and polypeptides of the invention are useful as
- 30      reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, vascular conditions where unwanted angiogenesis occurs such as retinopathy and in conditions such as restenosis and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are in providing immunological probes for
- 35      differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vascular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell

types (e.g., vascular tissue, endothelial cells, and dendritic cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 55 as residues: Lys-21 to Met-52, Asp-179 to Ala-189, Asp-194 to Val-202, Ile-205 to Asn-212.

The tissue distribution and homology the *Xenopus laevis* gene indicates that polynucleotides and polypeptides corresponding to the gene are useful for treatment/diagnosis of problems involving the vascular system since expression is in endothelial cells.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 6

This gene is expressed primarily in an endometrial tumor and to a lesser extent in skin tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, tumors, in particular, skin and endometrial tumors. Similarly, polypeptides and antibodies directed to these polypeptides are in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skin and reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., endometrium, and epidermis, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to the gene are useful for treatment/diagnosis of endometrial and/or skin tumors, based on levels of expression in these tissues.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 7

This gene is expressed primarily in human neutrophils and to a lesser extent in fetal liver.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancers of the immune system and/or liver. Similarly, polypeptides and antibodies directed to these polypeptides are in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune or hepatic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and liver, and cancerous and wounded tissues)
- 5      or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.
- 10     The tissue distribution indicates that polynucleotides and polypeptides corresponding to the gene are useful for regulation of cell division or treatment of cancers, particularly of the immune and hepatic systems.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 8

- This gene is expressed primarily in various regions of the brain including corpus callosum and hippocampus and amygdala and to a lesser extent in multiple other tissues.
- 20     Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, diseases of the central nervous system including ischemia, epilepsy, Parkinson's disease or any other disease where neuronal survival is decreased.

- 25     Similarly, polypeptides and antibodies directed to these polypeptides are in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., brain and other tissue of the nervous system, and amygdala, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the
- 30
- 35

disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 58 as residues: Ser-11 to His-21.

- The tissue distribution suggests that polynucleotides and polypeptides corresponding to the gene are useful for treatment/diagnosis of conditions or diseases  
5 relating to the central nervous system based on the expression in various tissues of the brain.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 9

- The translation product of this gene shares sequence homology with a  
10 thioredoxine homolog from *C. elegans* which possesses dithiol-disulfide oxidoreductase activity. Preferred polypeptide fragments comprise the amino acid sequence: DGNPCDFDWREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVAN TILFFRLDIRMGLLYITLCIVFLMTCKPPLYMGPEYIKYFNDKTIDEELERDKRVT WIVEFFANWSNDCQSFAPIYADLSLKYNCTGLNGKVDVGRYTDVSTRYKVST  
15 SPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVS WTFSEENVIREFNLNEL YQRA KKLSKA (SEQ ID NO:92). Polynucleotides encoding these polypeptide fragments are also encompassed by the invention.

- This gene is expressed primarily in fetal liver and to a lesser extent in other tissue.  
20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, developmental diseases including problem with early hematopoiesis. Similarly, polypeptides and antibodies directed to these polypeptides are in providing  
25 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., liver, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or  
30 cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 59 as residues: Pro-50 to Phe-61, Glu-148 to Arg-155, Thr-200 to Ser-209, Arg-232 to Gly-239, Gln-262 to Ser-268, Ala-270 to Val-  
35 280.

The tissue distribution and homology to thiooxidase suggests that polynucleotides and polypeptides corresponding to the gene are useful for treatment of disorders involving protein folding abnormalities and diagnosis/treatment of developmental or hematopoietic disorders.

5

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 10**

This gene is expressed primarily in T-cells and to a lesser extent in smooth muscle. This gene maps to chromosome 14, and therefore can be used in linkage analysis as a marker for chromosome 14.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, diseases of immune dysfunction such as inflammation and autoimmunity including rheumatoid arthritis and Lupus. Similarly, polypeptides and  
15 antibodies directed to these polypeptides are in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., T-cells, and smooth muscle, and cancerous and wounded tissues) or bodily  
20 fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 60 as residues: Ala-3 to Thr-9, Ser-40 to Asn-53, Ser-  
25 59 to Asp-85, Gly-89 to Thr-100.

The tissue distribution suggests that polynucleotides and polypeptides corresponding to the gene are useful for treatment/diagnosis of immune and inflammatory diseases.

30 **FEATURES OF PROTEIN ENCODED BY GENE NO: 11**

The translation product of this gene shares sequence homology with a W04A4.5 protein found in the *Caenorhabditis elegans* genome (See Accession NO: 2414330). Preferred polypeptide fragments comprise the amino acid sequence: IHLALVELLKNL TKYPTDRDSIWKCLKFLGSRHPTLVLPLVPELLSTHPFFDTAEPDMDDPAYIAVL  
35 VLIFNAAKTCPTMPALFSDHTFRHYAYLRDSLSHLVPALRLPGRKLVSSAVSPSI IPQEDPSQQFLQQSLERVYSLQHLDPPQGAQELLEFTIRDLQRLGELQSELAGVAD

FSATYLRQQLLIKALQEKLWNVAAPLYLKQSDLASAAAKQIMEETYKMEFMY  
SGVENKQVIIHHMRLQAKALQLIV (SEQ ID NO:94); or QLIVTARTTRGLDPLF  
GMCEKFLQEVDFFQRYFIADLPHLQDSFVDKLLDLMPRLMTSKPAEVVKILQTM  
LRQSAFLHLPLPEQIHKASATIIEPAGEFRQPFAVYLWVGGCPGMLMQPWNSMC

- 5 RILRTLLRSRVLYPDGQXSDDSPQACRLPESWPRAAPAHSGLSLPHRLDRGM  
PGGSEAAAGLQLQCSHSKMP (SEQ ID NO:93). Polynucleotides encoding this  
polypeptide are also encompassed by the invention. Based on the conserved homology  
between invertebrate and human, it is likely that this gene plays an essential role in the  
development or the functions of human and animal body. This gene maps to  
10 chromosome 11, and therefore can be used in linkage analysis as a marker for  
chromosome 11.

This gene is expressed primarily in hypothalamus and other brain tissues and to  
a lesser extent in human breast, colon carcinoma, and cells of T-cell origin including T-  
cell lymphoma.

- 15 Therefore, polynucleotides or polypeptides of the invention are useful as  
reagents for differential identification of the tissue(s) or cell type(s) present in a  
biological sample and for diagnosis of diseases and conditions which include, but are  
not limited to disorder, inflammatory and immune disorders, cancers involving cells of  
lymphoid origin, or other infected or neoplastic lesions with T-cell infiltration.  
20 Similarly, polypeptides and antibodies directed to these polypeptides are in providing  
immunological probes for differential identification of the tissue(s) or cell type(s). For a  
number of disorders of the above tissues or cells, particularly of the immune and central  
nervous system including autoimmune disorders, expression of this gene at  
significantly higher or lower levels may be routinely detected in certain tissues and cell  
25 types (e.g., brain and other tissue of the nervous system, mammary tissue, colon, T-  
cells, lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g.,  
serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample  
taken from an individual having such a disorder, relative to the standard gene  
expression level, i.e., the expression level in healthy tissue or bodily fluid from an  
30 individual not having the disorder.

- The tissue distribution in the hypothalamus indicates that the protein product of  
this clone is an endocrine or an extracellular protein regulatory factor in nature. The  
abundant presence in the brain tissues may indicate its involvement in neural  
development, such as neuronal survival and maintenance, neuronal connection and  
35 axonal guidance, in neural physiology, such as neural impulses transmission, short  
term and long term potentiation, or signal quenching. Furthermore, the gene product

may have functions outside the nerve tissues as it is often found in tissues with T-cell enrichment. For example, in the lesions of colon carcinoma, breast cancer, bone marrow cells, T-cell lymphoma, activated T-cells, and tissues or cells of immune importance, the gene expression levels are significant, which indicate the 5 immunological involvement, likely cellular immunity in nature. Therefore polynucleotides and polypeptides corresponding to the gene are useful for treatment or diagnosis of disorders of the endocrine system, neural dysfunctions or neurodegeneration, immune or inflammatory diseases, or as a proliferative/differentiation agent for cells of lymphoid origin.

10

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 12

The translation product of this gene shares sequence homology with a 27-kDa protein (mouse transporter protein (MTP)) with four predicted transmembrane-spanning domains, which is thought to be important in the transport of nucleosides and/or 15 nucleoside derivatives between the cytosol and the lumen of an intracellular membrane-bound compartment. Preferred polypeptide fragments comprise the amino acid sequence: RFYSNSCCLCCHVRTGTILLGVWYLIINAVVLLILLSALADPDQYNFS SSELGGDFEFMDANMCIAIAISLLMILICAMATYGAYKQRAAGIIPFFCYQIFDF ALNMLVAITVLIYPNSIQEYIRQLPPNFPYRDD (SEQ ID NO:95); or FPTEEMMSCA 20 VNPTCLVLIILLFISIILTAKGYLISCVWNCYRYINGRNSSDVLVYVTSNDTVLL PPYDDATVNGAAKEPPPPYVSA (SEQ ID NO: 96). Polynucleotides encoding these polypeptides are also encompassed by the invention. It is likely that a second signal sequence is located upstream from the predicted signal sequence. Moreover, it is likely that a frame shift exists, which can easily be clarified using known molecular biology 25 techniques.

This gene is expressed primarily in an endometrial tumor and normal ovary and to a lesser extent in a stromal cell line, T-cells and other cancer tissues including skin, testes chondrosarcoma, and synovial sarcoma .

Therefore, polynucleotides and polypeptides of the invention are useful as 30 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer, particularly of the female reproductive organs and inflammatory and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are in providing immunological probes for differential identification of the 35 tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the female reproductive and immune], expression of this gene at

- significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., ovary and testes and other reproductive tissue, stromal cells, and T-cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual
- 5 having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to the MTP transporter gene suggests that polynucleotides and polypeptides corresponding to the gene are useful for

10 treatment/diagnosis of certain cancers by blocking the ability to utilize nucleotide and nucleoside derivatives, and may also be useful modulation of immune responses by regulating the transport of these molecules.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 13

- 15 The translation product of this gene shares sequence homology with a mouse cysteine-rich glycoprotein/mouse monocyte surface antigen (MS2 precursor). (See Accession NO: 1709103.) Moreover, another group recently cloned this gene, calling it human MS2, a myelomonocytic cell surface protein. (See Accession NO: 1864005.) This transmembrane protein is a member of the hemorrhagic snake venom family.
- 20 Thus, based on homology, it is likely that this gene have activity similar to monocyte or myelomonocyte surface antigen M2S. Preferred polypeptide fragments comprise the amino acid sequence: IAPSRPWALMEQYEVVLPWRLPGPRVRRALPSHLGLHPE RVSYVLGATGHNFTLHLRKNRDLLGSGYTETYTAANGSEVTEQPRGQDHCFY QGHLEG (SEQ ID NO:97); PDSAASLSTCAGLRGFFQVGSDLHLIEPLDEGGEGG
- 25 RHAJVYQAEHLLQTAGTCGVSDDSLGSLLGPRTAAVFRPRPGDSLPSRETRYVEL YVVVDNAEFQMLGSEAAVRHRVLEVNVHDVKLYQKLNFRVVLVGLEIWNNSQD RFHVSPDPVTLENLLTWQARQRTRRHLHDNVQLITGVDFGTGTVGFARVSAM CSHSSGAVNQDHSKNPVGVACTMAHE MGHNLGMDHDENVQGCRCQ (SEQ ID NO:98); and/or FEAGRCIMARPALAPSFPRMFSDCSQAYLESFLERPQSVCIA
- 30 NAPDLSHLVGGPVCGNLFVERGEQCDCGPPEDCRNRCNCNSTCQLAEGAQCIA HGTCCQECKVKPAGELCRPKKDMC (SEQ ID NO:99). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in human eosinophils and human tonsils.

- Therefore, polynucleotides or polypeptides of the invention are useful as
- 35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are

- not limited to, disorders relating to eosinophilic leukocyte, and tonsillitis. Similarly, polypeptides and antibodies directed to these polypeptides are in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic
- 5 system and lymphoid system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and tonsils, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,
- 10 the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of immune disorders.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 14**

A polypeptide sequence which overlaps with the translation product of this gene has recently been identified as g16 (see Genbank accession NO: gil2636658). These proteins are thought to be tumor suppressors.

- This gene is expressed primarily in immune system cells, e.g., eosinophils,
- 20 activated T-cells, activated monocytes, activated neutrophils, dendritic cells, Hodgkin's lymphoma, and in vascularized tissues such as umbilical vein, microvascular endothelial cells and trachea.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

25 biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune system disorders such as cancer. Similarly, polypeptides and antibodies directed to these polypeptides are in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and immune systems,

30 expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, dendritic cells, vascular tissue, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,

35 the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and similarity to g16 suggests that polynucleotides and polypeptides corresponding to the gene are useful for diagnosis and treatment of immune system disorders such as cancers. It is believed that tumor suppressor genes are often deleted in particular cancers.

5

### FEATURES OF PROTEIN ENCODED BY GENE NO: 15

The translation product of this gene shares sequence homology with a frog thrombin receptor [Xenopus laevis]. Moreover, another group recently cloned this same gene, also recognizing the homology to thrombin receptors. (See Accession NO:

- 10 2347084.) Preferred polypeptide fragments comprise the amino acid sequence: MLPD WKXSLILMAYIIIFLTGLPANLLALRAFVGRIRQPQPAWPVHILLSLTLADLLLLL  
LPFKIIEAASNFRWYLPKVVCAUTSGFYSSIYCSTWLLAGISIERYLGVAFPVQ  
YKLSRRPLYGVIAALVAWVMSFGHCTIVIIXQYLNTTEQVRSGNEITCYENFTD  
NQLDVVLPPRXELCLVLFFXPMAVTIFCYWRFVWIMLSQPLVGQAQRRAVGL  
15 AVVTLLNFLVCFGPYNVSHLVGYHQRKSPWWRSIAVXFSSLNASLDPLLKYFS  
SSVVRRRAFGRGLQVLRNQGSSLLGRRGKDTAEGTNEDRGVGQGEQMPSSDFT  
TE (SEQ ID NO:100); CSTWLLAGISIERYLGV (SEQ ID NO:101); or CTIVIIXQYL  
NTTEQVRSGNEITCYENFTDNQLDVVLPPRXELCLVLFFXPMAVTIFCYWRFV  
WIMLSQPLVGQAQRRAVGLAVVTLLNFLVC (SEQ ID NO:102).

- 20 Polynucleotides encoding these polypeptides are also encompassed by the invention.

Also preferred are the polynucleotide fragments encoding these polypeptide fragments. This gene maps to chromosomal location 19q13.1, and therefore can be used as a marker in linkage analysis for chromosome 19.

- 25 This gene is expressed primarily in activated human neutrophil and IL5 induced eosinophil.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, neutropenia, neutrophilia, and eosinophilic leukocyte related disorders.

- 30 Similarly, polypeptides and antibodies directed to these polypeptides are in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic system and hemopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone marrow, blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an

individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 65 as residues: Tyr-41 to Trp-48.

- 5        The tissue distribution a suggests that polynucleotides and polypeptides corresponding to the gene are useful for diagnosis and treatment of immune disorders.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 16

- This gene is homologous to the mouse NP15.6 gene, a novel neuronal protein  
10      whose expression is developmentally regulated. (See Accession NO: 1771306.) Therefore, based on homology, it is likely that this gene would have activity similar to NP15.6. Preferred polypeptide fragments comprise the amino acid sequence:  
GLPAARVRWESSFSRTVVAPSAVAXKRPEPTTPQEDPEPEDENLYEKNPDS  
HGYDKDPVLVDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRCTGCPRAWDGMK  
15      EWSRREAERLVKYREANGLPIMESNCFDPSKIQLPEDE (SEQ ID NO:103).  
Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene maps to chromosome X, and therefore polynucleotides of the present invention can be used in linkage analysis as a marker for chromosome X.

- This gene is expressed primarily in hematopoietic cells.  
20      Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are in providing immunological probes for differential identification 25      of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., hematopoietic cells, and tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or  
30      another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 66 as residues: Pro-24 to Gly-30, Gly-37 to Ala-46.  
35      The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of immune and endocrine disorders and neoplasias.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 17**

- The translation product of this gene shares sequence homology with Preprotachykinin B which is thought to be important in the signal transduction and information processing in the nervous system. (See Accession NO:163590; see also Kotani,H., et al., Proc. Natl. Acad. Sci. U.S.A. 83:7074-7078 (1986).) The tachykinin group of neuropeptides exists in four different forms which are derived from one gene in the rat. Alternative splicing accounts for the alpha, beta, gamma, and delta forms. The most famous of these neuropeptides is substance P which appears to mediate the pain sensation and wheal formation in certain *in vivo* models. It thus may be a key player in the inflammatory response. The tachykinins also have smooth muscle contraction (i.e. bronchoconstriction) and vasodilator effects. Additionally, neovascularization and various cell-type specific proliferation effects have been seen. The fact that this clone was isolated from placenta RNA may make this an interesting gene to characterize. The known neurokinins are expressed in either the central nervous system or peripheral neurons. It may be that this new neurokinin modulates smooth muscle or vascularization associated with reproduction. Therefore, base on homology it is likely that the polypeptides of the invention are active in the signal transduction and information processing in the nervous system. Preferred polypeptide fragments comprise the amino acid sequence: PEKRDMDFFVGLMGKRSVQPDSPTDVNQE NVPSFG (SEQ ID NO:104); KRDMHDFFVGLMGKR (SEQ ID NO:105); and/or DMHDFFVGLM (SEQ ID NO:106). Polynucleotides encoding these polypeptides are also encompassed by the invention. This maps to chromosome 12 and therefore can be used in linkage analysis as a marker for chromosome 12.
- This gene is expressed primarily in human placenta and to a lesser extent in soares placenta.
- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, embryonic and reproductive disorders. Similarly, polypeptides and antibodies directed to these polypeptides are in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive and embryonic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., placenta, and tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal

- fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 67 as residues: Gly-34 to Asp-42, 5 Ala-67 to Asp-81, Arg-93 to Asn-107.

The tissue distribution and homology to preprotachykinin B suggests that polynucleotides and polypeptides corresponding to the gene are useful for the diagnosis and treatment of reproductive and embryonic disorders, and cancer. These polypeptides and polynucleotides of the invention can also be used to treat Alzheimer's 10 disease by inhibition of neurotoxicity due to the beta-amyloid peptide and long-lasting analgesic and anti-inflammatory activities by neurokinin B analogs.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 18**

- The translation product of this gene shares sequence homology with ftp-3, an 15 hnRNP protein which is thought to be important in RNA splicing and packaging. In preferred embodiments, the polypeptides of the invention comprise the sequence: EWEATEEMEWEIIREAM (SEQ ID NO:107); WEWGTITVEDMVLLMVWWVMAVV VEADEVTMGKAA (SEQ ID NO:108); GMGGYGRDGMDNQGGYGS (SEQ ID NO:109); and/or GMGNYYSGGYGTPDGLGGYGRGGGGSGGGYYGQGGMSGG 20 GWRGM (SEQ ID NO:110). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in frontal cortex and amygdala of human brain and to a lesser extent in human smooth muscle.

- Therefore, polynucleotides and polypeptides of the invention are useful as 25 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, human brain diseases. Similarly, polypeptides and antibodies directed to these polypeptides are in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, 30 particularly of the nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., brain and other tissue of the nervous system, and smooth muscle, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard 35 gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to ftp-3 indicates that the protein product of this clone is useful for the diagnosis and treatment of human brain diseases and disorders involving improper RNA splicing such as thalessemia. Additionally, this gene maps to chromosome 10 and therefore polypeptides of the present invention can be  
5 used in linkage analysis as a marker for chromosome 10.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 19**

The translation product of this gene shares sequence homology with immunoglobulin lambda light chain which is thought to be important in immunal  
10 functions.

This gene is expressed primarily in human thymus and to a lesser extent in human colon, soares breast, bone marrow and breast lymph node.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a  
15 biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immunal diseases. Similarly, polypeptides and antibodies directed to these polypeptides are in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system expression of this gene at significantly higher or  
20 lower levels may be routinely detected in certain tissues (e.g., thymus, colon, mammary tissue, bone marrow, and lymphoid tissue, and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an  
25 individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 69 as residues: Gly-43 to Asp-50, Gln-57 to Lys-65, Arg-70 to Gly-77, Thr-185 to Tyr-195, Pro-205 to Ser-215.

The tissue distribution and homology with immunoglobulin lambda light chain indicates that polynucleotides and polypeptides corresponding to the gene are useful for  
30 the diagnosis and/or treatment of immunal diseases.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 20**

The translation product of this gene shares sequence homology with *Xenopus* chordin (Accession NO:L35764) which is thought to be important in dorsal-ventral patterning and is activated by organizer-specific homeobox genes. See, e.g., Sasai,Y.,  
35

et al., Cell 79:779-790 (1994).) This gene has also been determined to be a powerful morphogen.

This gene is expressed primarily in early stage human tissues, prostate, and adipose tissues and to a lesser extent, in other tissues.

- 5       Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, developmental disorders. Similarly, polypeptides and antibodies directed to these polypeptides are in providing immunological probes for differential 10 identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the embryo and fetal tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., embryonic and fetal tissue, prostate, and adipose tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or 15 another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 70 as residues: Asn-28 to Trp-38, Val-57 to Lys-64, His-66 to Lys-82, Glu-90 to Gly-100, Glu-210 to Cys-217.
- 20       Chordin plays important role dorsal-ventral patterning in *Xenopus*. The tissue distribution and homology to chordin suggests that polynucleotides and polypeptides corresponding to the gene are useful for diagnosis and treatment of wounds and developmental disorders, such as cancer.

25       **FEATURES OF PROTEIN ENCODED BY GENE NO: 21**

This gene is expressed primarily in immune tissues such as monocyte, fetal liver, fetal spleen, T-cell, thymus etc. and to a lesser extent in colon cancer, breast cancer, early stage human tissues and a few other tissues.

- 30       Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune disorders such as immune deficiencies, autoimmune diseases, and inflammatory diseases. Similarly, polypeptides and antibodies directed to these polypeptides are in providing immunological probes for differential identification of the 35 tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune systems, expression of this gene at significantly higher or

lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, liver, spleen, thymus, colon, and mammary tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to  
5 the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 71 as residues: Glu-61 to Thr-67, Glu-72 to Asp-81, Glu-83 to Asp-118, Gly-156 to Arg-162, Asp-184 to Tyr-205, Met-251 to Asp-257, Ser-284 to Tyr-293, Lys-351 to Arg-357, Gly-367 to Asp-375, Asn-399  
10 to Glu-414, Gln-424 to Arg-443, Glu-447 to Glu-457, Arg-462 to Lys-476, Lys-485 to Phe-492.

The tissue distribution suggests that polynucleotides and polypeptides corresponding to the gene are useful for diagnosis and treatment of immune disorders such as immune deficiencies, autoimmune diseases, and inflammatory diseases.

15

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 22**

In one embodiment of the invention, the polypeptides of the invention comprise the sequence FTHSFILEHAFSLLITLPVSSWAANN (SEQ ID NO:111).

20

This gene is expressed primarily in chronic synovitis and to a lesser extent in other tissues.

25

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of chronic synovitis. Similarly, polypeptides and antibodies directed to these polypeptides are in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the synovium, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., synovial tissue and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to  
30 the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution suggests that polynucleotides and polypeptides corresponding to the gene are useful for diagnosis and treatment of chronic synovitis.

35

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 23**

This gene is expressed primarily in testes and to a lesser extent in other tissues.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, testes related diseases such as infertility and endocrine disorders.
- 5     Similarly, polypeptides and antibodies directed to these polypeptides are in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the testes, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., testes and other reproductive tissue, and cancerous and wounded tissues)
- 10    or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.
- The tissue distribution suggests that polynucleotides and polypeptides
- 15    corresponding to the gene are useful for diagnosis and treatment of testes related diseases such as infertility and endocrine disorders.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 24

The translation product of this gene shares sequence homology with the nucleotide sequence of a new HLA-DRB1(\*)11 allele (DRB1(\*)1124), which is thought to be important in organ transplantation and immune disorders. The translation product of this gene also shares homology with protease inhibitors such as aprotinin and others with Kunitz-type domains. Kunitz-type domains are known in the art to possess protease inhibiting activity. A Kunitz-type domain is contained within the translation product of this gene and has the amino acid sequence: CEMPKETGPCLAY FLHWWYDKKDNTCSMFVYGGCQGNNNNFQSKANCLNTC (SEQ ID NO:112). Thus, preferred polypeptides of the invention comprise the amino acid sequence of the Kunitz-type domain shown immediately above.

It has been discovered by analyzing hundreds of thousands of ESTs that this gene is expressed primarily in the testes and epididymus. Northern blot analysis has confirmed expression primarily in the testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, diseases related to the testes and epididymus. Similarly, polypeptides and antibodies directed to these polypeptides are in providing immunological probes for

differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the diseases related to the testes and epididymus, and organ transplantation. expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., testes and other

- 5 reproductive tissue, and tissue and cells of the immune system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include
- 10 those comprising a sequence shown in (SEQ ID NO:74) as residues: Pro-30 to Arg-37, Val-47 to Lys-59, Trp-94 to Thr-101, Cys-110 to Cys-123, Thr-126 to Pro-133.

The tissue distribution and homology to protease inhibitors indicates that polynucleotides and polypeptides corresponding to the gene are useful for diagnosis and treatment of diseases related to the testes, epididymus, and organ transplantation.

- 15 More specifically, these polypeptides are particularly useful in the treatment of hyperfilbrinolytic hemorrhage and traumatic hemorrhagic shock as well as in diseases connected with excessive release of pancreatic elastase (pancreatitis), serum elastase (atherosclerosis), leukocyte elastase in acute and chronic inflammation with damage to connective tissue, in damage to vessel walls, in necrotic diseases, and degeneration of
- 20 lung tissue.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 25**

The translation product of this gene shares sequence homology with CpG islands genes which are short stretches of DNA containing a high density of non-methylated CpG dinucleotides, predominantly associated with coding regions. As CpG islands overlap with approximately 60% of human genes, the CpG island library can be used to isolate full-length cDNAs and to place genes on genomic maps.

This gene is expressed primarily in the testes and to a lesser extent in the lung, tonsils, placenta, and rhabdomyosarcoma.

- 30 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, diseases related to the testes, lung, tonsils, placenta, and tumors. Similarly, polypeptides and antibodies directed to these polypeptides are in providing
- 35 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the diseases related to

the testes, lung, tonsils, placenta, and tumors, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., testes and other reproductive tissue, lung, tonsils, placenta, and striated muscle, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal

- 5 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:75 as residues: Met-1 to His-7.

The tissue distribution indicates that polynucleotides and polypeptides  
10 corresponding to the gene are useful for diagnosis and treatment of diseases related to the testes, lung, tonsils, placenta, and tumors.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 26

The translation product of this gene shares sequence homology with the  
15 sequence of human villin: a large duplicated domain homologue with other actin severing proteins and a unique small carboxy terminal domain related to villin specificity which is thought to be important in actin capping and processing. This gene has now been published. See DNA Res. (1997) 28:4(1):35-43. It has been shown that this gene is homozygously deleted in a lung carcinoma cell line suggesting a possible role for the  
20 translation product of this gene in suppressing tumors. In any case, a suppressor gene is likely located close to this gene and accordingly, this gene can be used as a cancer marker. Preferred polypeptides of this invention comprise the following amino acid sequence: MMIQWNGPKTSISEKARGLXLTYSLRDRERGGGRAQIGVVDDEAKA  
PDLMQIMEVLGRRVGXLRXATPSKDINQLQKANVRLYHVYEKGKDLVVLELA  
25 TPPLTQDLLQEEDFYILDQGGFKIYVWQGRMSSLQERKAAFSRAVGFIQAKGYP  
TYTNVEVVNDGAESAAFKQLFRTWSEKRRRNQKXGGRDKSIHVKLDVGKLH  
TQPKLAAQLRMVDDGSGKVEVWCICQDLHRQPVDPKRHGQLCAGNCYLVLYTY  
QRLGRVQYILYLWQGHQATADEIEALNSNAEELDVMYGGVLVQEHTMGSEPP  
HFLAIFQGQLVIFQERAGHHGKGQSASTRLFQVQGTDHSNTRTMEVPARASS  
30 LNSSDIFLLVTASVCYLWFGKG (SEQ ID NO:113).

It has been discovered by analyzing EST sequences that this gene is expressed primarily in a healing wound 7.5 hours after incision, pancreas tumor, CD34+ cell, human osteoclastoma, stromal cells, human thymus and to a lesser extent in pancreas tumor, spleen, and apoptotic T cell. Northern blots were carried out and showed that  
35 this gene was expressed in all tissues tested: spleen, thymus, prostate, testis, ovary, small intestine, colon, and peripheral blood leukocytes. The most intense band

(expression) was seen in the colon, with the least intense band seen in peripheral blood leukocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancers including, lung carcinoma, osteoclastoma, pancreas tumor, immune disorders, and infectious diseases. Similarly, polypeptides and antibodies directed to these polypeptides are in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone, stromal cells, thymus, pancreas, lung, spleen, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to the Villin family of actin severing proteins suggests that polynucleotides and polypeptides corresponding to the gene are useful for diagnosis and treatment of cancers, particularly osteoclastoma, pancreas tumor, lung carcinoma, other immune disorders, and infectious diseases. It has recently been shown that sputum samples from cystic fibrosis patients contains actin filaments and that plasma gelsolin can reduce the viscosity of these samples. Accordingly, the translation product of this gene is useful in the treatment of cystic fibrosis. This gene has been mapped to 3p22-p21.3.

25

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 27

This gene is expressed primarily in a human HCC cell line, mouse liver metastasis and muscle tissue from a human patient with multiple sclerosis.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, tumor metastasis and multiple sclerosis. Similarly, polypeptides and antibodies directed to these polypeptides are in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.,

liver, and muscle, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:77 as residues: Ser-21 to Asp-32.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to the gene are useful for diagnosis and treatment of multiple sclerosis and tumor metastasis. The nucleotide sequence 3' of the poly A tail, as shown in the sequence listing is vector sequence as would be readily appreciated by those of skill in the art. Polypeptides of the invention preferably do not contain such vector sequences or sequences which hybridize to such vector sequences.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 28

15 The translation product of this gene shares sequence homology with the sequence CEESL52F (Genbank accession NO: U80441); coded for by *C. elegans* cDNA yk5 which is thought to be important in embryonic development. The translation product of this gene has recently been described elsewhere (See Proc. Natl. Acad. Sci. U S A (1997) 8:94(14):7481-7486, incorporated herein by reference in its entirety), as  
20 hCTR2: a human gene for copper uptake.

This gene is expressed primarily in placenta and human amygdala, and to a lesser extent in adult brain, primary dendritic cells, keratinocytes, activated monocytes, human cerebellum, and activated T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as  
25 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, embryonic development, neuronal cell differentiation, disorders associated with copper metabolism and immune responses. Similarly, polypeptides and antibodies directed to these polypeptides are in providing immunological probes for  
30 differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the abnormal embryonic development, neuronal cell disorders, disorders involving abnormal copper metabolism and immune system disorders, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., placenta, amygdala, brain and other tissue of  
35 the nervous system, dendritic cells, blood cells, keratinocytes, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal

fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 78 as residues: Ser-24 to Trp-30.

5       The tissue distribution and similarity to hCTR1 and hCTR2 indicates that polynucleotides and polypeptides corresponding to the gene are useful for diagnosis and treatment of abnormal embryonic development, neuronal cell disorders, disorders involving copper metabolism and immune system disorders. This gene has been mapped to 9q31-q32.

30

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	NT SEQ ID NO: X	NT Total NT Seq.	5' NT of Clone Seq.	3' NT of Start Codon	5' NT of AA of Signal Pep.	NT SEQ ID NO: Y	AA of Sig Pep.	First AA of Sig Pep.	Last AA of Sig Pep.	First AA of Secreted Portion	Last AA of ORF
1	HCEAB46	97921 03/07/97	Uni-ZAP XR	11	2084	695	2084	908	908	51	1	27	28
2	HCEDH81	97921 03/07/97	Uni-ZAP XR	12	1586	1	1586	72	72	52	1	1	2
2	HCEDH81	97921 03/07/97	Uni-ZAP XR	39	1907	1	1907	1211	1211	79	1	16	17
3	HCEDO84	97921 03/07/97	Uni-ZAP XR	13	2350	1800	2328	1666	1666	53	1	37	38
4	HCUHF89	97921 03/07/97	ZAP Express	14	1348	955	1348	976	976	54	1	33	34
5	HELDY41	97921 03/07/97	Uni-ZAP XR	15	1123	1	1123	41	41	55	1	20	21
5	HELDY41	97921 03/07/97	Uni-ZAP XR	40	1114	1	1114	19	19	80	1	21	22
6	HETDM20	97921 03/07/97	Uni-ZAP XR	16	890	19	772	134	134	56	1	40	41
7	HFVGR41	97921 03/07/97	pBluescript	17	619	63	619	198	198	57	1	27	28
8	HIBCO28	97921 03/07/97	Other	18	1768	15	1768		1	58	1	17	18
9	HJBCD89	97921 03/07/97	pBluescript SK-	19	1699	23	1679	30	30	59	1	48	49
9	HJBCD89	97921 03/07/97	pBluescript SK-	41	1652	16	1652		1	81	1	42	43
													293

3 1

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	NT SEQ ID	5' NT of Total NT Seq. NO: X	3' NT of Clone Seq. NO: Y	5' NT of AA of Signal Pep	AA SEQ ID	First AA NO: Y	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
10	HJTAAl7	97921 03/07/97	Lambda ZAP II	20 736	85	685	123	60	1	32	33 100
11	HLTBS22	97921 03/07/97	Uni-ZAP XR	21 1688	1	1682	186	61	1	21	22 47
12	HTEBY84	97921 03/07/97	Uni-ZAP XR	22 2045	76	1980	221	62	1		13
13	HNFCV70	97922 03/07/97 209070 05/22/97	Uni-ZAP XR	23 1101	77	1101	96	63	1	21	22 335
13	HNFCV70	97922 03/07/97 209070 05/22/97	Uni-ZAP XR	42 1473	1	1473	50	50	82	1	20 21 143
14	HNFEY18	97922 03/07/97 209070 05/22/97	Uni-ZAP XR	24 1659	1	1659	1378	1378	64	1	18
15	HNFGF45	97922 03/07/97 209070 05/22/97	Uni-ZAP XR	25 1329	4	1329	696	696	65	1	37 38 125
16	HUSAQ32	97922 03/07/97 209070 05/22/97	Lambda ZAP II	26 700	47	609	280	280	66	1	18 19 77

32

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	NT SEQ ID	Total NT Seq. X	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
17	HPMBQ91	97922 03/07/97 209070 05/22/97	Uni-ZAP XR	27	832	1	832	141	141	67	1	16
17	HPMBQ91	97922 03/07/97 209070 05/22/97	Uni-ZAP XR	43	772	1	772	127	127	83	1	18
18	HOEBI94	209083 05/29/97	Uni-ZAP XR	28	2361	411	2285	596	596	68	1	17
18	HRSAJ18	97922 03/07/97 209070 05/22/97	ZAP Express	44	403	69	403	111	111	84	1	18
19	HRSMC69	97922 03/07/97 209070 05/22/97	ZAP Express	29	879	565	879	13	13	69	1	21
19	HRSMC69	97922 03/07/97 209070 05/22/97	ZAP Express	45	928	204	418		381	85	1	4
19	HBM SH54	209551 12/12/97	Uni-ZAP XR	46	885	1	885	21	21	86	1	22
											23	235

c4  
c3

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	NT SEQ ID	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	AA SEQ ID	First AA of Signal Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
			Total NT Seq.	NO: X			NO: Y				
20	HSDEG01	97922 03/07/97 209070 05/22/97	Uni-ZAP XR	30	1732	1	1732	267	70	1	30
20	HSDEG01	97922 03/07/97 209070 05/22/97	Uni-ZAP XR	47	2315	1	2315	2055	87	1	21
21	HSQFP46	97922 03/07/97 209070 05/22/97	Uni-ZAP XR	31	3259	1299	2170	238	71	1	20
21	HSQFP46	97922 03/07/97 209070 05/22/97	Uni-ZAP XR	48	3175	1118	1941	1565	88	1	32
22	HSVCB57	97922 03/07/97 209070 05/22/97	Uni-ZAP XR	32	454	1	454	61	72	1	18
23	HTEAE62	97922 03/07/97 209070 05/22/97	Uni-ZAP XR	33	230	27	162	7	73	1	21

54

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	NT SEQ ID NO: X	NT Total Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT Start Codon	AA of Signal Pep	First SEQ ID NO: Y	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
24	HTEBY11	97922 03/07/97 209070 05/22/97	Uni-ZAP XR	34	753	43	753	31	31	74	1	21
24	HTEBY11	97922 03/07/97 209070 05/22/97	Uni-ZAP XR	49	783	30	783	254	254	89	1	29
25	HTEEB42	97922 03/07/97 209070 05/22/97	Uni-ZAP XR	35	1022	20	1022	59	59	75	1	22
26	HTPBY11	97922 03/07/97 209070 05/22/97	Uni-ZAP XR	36	3044	1	3035	336	336	76	1	2
26	HTPBY11	97922 03/07/97 209070 05/22/97	Uni-ZAP XR	50	3030	1	3030	1908	1908	90	1	31
27	H2MBT68	97922 03/07/97 209070 05/22/97	pBluescript SK-	37	541	4	341	187	187	77	1	23
											24	39

Gene No.	CDNA Clone ID	ATCC Deposit Nr and Date	NT SEQ ID	NT Total Seq. NO: X	5' NT of Clone Seq.	3' NT of Seq.	5' NT Start Codon	First AA of Signal Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
28	HAGAI85	97922 03/07/97 209070 05/22/97	Uni-ZAP XR	38	1752	52	1752	166	166	78	1

Table 1 summarizes the information corresponding to each "Gene No." described above. The nucleotide sequence identified as "NT SEQ ID NO:X" was assembled from partially homologous ("overlapping") sequences obtained from the "cDNA clone ID" identified in Table 1 and, in some cases, from additional related DNA clones. The overlapping sequences were assembled into a single contiguous sequence of high redundancy (usually three to five overlapping sequences at each nucleotide position), resulting in a final sequence identified as SEQ ID NO:X.

The cDNA Clone ID was deposited on the date and given the corresponding deposit number listed in "ATCC Deposit No:Z and Date." Some of the deposits contain multiple different clones corresponding to the same gene. "Vector" refers to the type of vector contained in the cDNA Clone ID.

"Total NT Seq." refers to the total number of nucleotides in the contig identified by "Gene No." The deposited clone may contain all or most of these sequences, reflected by the nucleotide position indicated as "5' NT of Clone Seq." and the "3' NT 15 of Clone Seq." of SEQ ID NO:X. The nucleotide position of SEQ ID NO:X of the putative start codon (methionine) is identified as "5' NT of Start Codon." Similarly, the nucleotide position of SEQ ID NO:X of the predicted signal sequence is identified as "5' NT of First AA of Signal Pep."

The translated amino acid sequence, beginning with the methionine, is identified 20 as "AA SEQ ID NO:Y," although other reading frames can also be easily translated using known molecular biology techniques. The polypeptides produced by these alternative open reading frames are specifically contemplated by the present invention.

The first and last amino acid position of SEQ ID NO:Y of the predicted signal peptide is identified as "First AA of Sig Pep" and "Last AA of Sig Pep." The predicted 25 first amino acid position of SEQ ID NO:Y of the secreted portion is identified as "Predicted First AA of Secreted Portion." Finally, the amino acid position of SEQ ID NO:Y of the last amino acid in the open reading frame is identified as "Last AA of ORF."

SEQ ID NO:X and the translated SEQ ID NO:Y are sufficiently accurate and 30 otherwise suitable for a variety of uses well known in the art and described further below. For instance, SEQ ID NO:X is useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in the deposited clone. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling a variety of forensic and diagnostic 35 methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used to generate antibodies which bind specifically to the secreted proteins encoded by the cDNA clones identified in Table 1.

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X and the predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing a human cDNA of the invention deposited with the ATCC, as set forth in Table 1. The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, or the deposited clone. The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

Also provided in the present invention are species homologs. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for the desired homologue.

The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below).

It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

- 5       The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified by the one-step method described in Smith and Johnson, Gene 67:31-40 (1988).  
Polypeptides of the invention also can be purified from natural or recombinant sources  
10      using antibodies of the invention raised against the secreted protein in methods which are well known in the art.

### Signal Sequences

Methods for predicting whether a protein has a signal sequence, as well as the cleavage point for that sequence, are available. For instance, the method of McGeoch, Virus Res. 3:271-286 (1985), uses the information from a short N-terminal charged region and a subsequent uncharged region of the complete (uncleaved) protein. The method of von Heinje, Nucleic Acids Res. 14:4683-4690 (1986) uses the information from the residues surrounding the cleavage site, typically residues -13 to +2, where +1 indicates the amino terminus of the secreted protein. The accuracy of predicting the cleavage points of known mammalian secretory proteins for each of these methods is in the range of 75-80%. (von Heinje, supra.) However, the two methods do not always produce the same predicted cleavage point(s) for a given protein.

In the present case, the deduced amino acid sequence of the secreted polypeptide was analyzed by a computer program called SignalP (Henrik Nielsen et al., Protein Engineering 10:1-6 (1997)), which predicts the cellular location of a protein based on the amino acid sequence. As part of this computational prediction of localization, the methods of McGeoch and von Heinje are incorporated. The analysis of the amino acid sequences of the secreted proteins described herein by this program provided the results shown in Table 1.

As one of ordinary skill would appreciate, however, cleavage sites sometimes vary from organism to organism and cannot be predicted with absolute certainty. Accordingly, the present invention provides secreted polypeptides having a sequence shown in SEQ ID NO:Y which have an N-terminus beginning within 5 residues (i.e., + or - 5 residues) of the predicted cleavage point. Similarly, it is also recognized that in some cases, cleavage of the signal sequence from a secreted protein is not entirely

uniform, resulting in more than one secreted species. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

Moreover, the signal sequence identified by the above analysis may not necessarily predict the naturally occurring signal sequence. For example, the naturally occurring signal sequence may be further upstream from the predicted signal sequence. However, it is likely that the predicted signal sequence will be capable of directing the secreted protein to the ER. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

10 **Polynucleotide and Polypeptide Variants**

"Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

- 15 "Identity" per se has an art-recognized meaning and can be calculated using published techniques. (See, e.g.: (COMPUTATIONAL MOLECULAR BIOLOGY, Lesk, A.M., ed., Oxford University Press, New York, (1988); BIocomputing: INFORMATICS AND GENOME PROJECTS, Smith, D.W., ed., Academic Press, New York, (1993); COMPUTER ANALYSIS OF SEQUENCE DATA, PART I, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, (1994); SEQUENCE ANALYSIS IN MOLECULAR BIOLOGY, von Heinje, G., Academic Press, (1987); and SEQUENCE ANALYSIS PRIMER, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, (1991).) While there exists a number of methods to measure identity between two polynucleotide or polypeptide sequences, the term "identity" is well known to skilled artisans. (Carillo, H., and Lipton, D., SIAM J Applied Math 48:1073 (1988).) Methods commonly employed to determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Huge Computers," Martin J. Bishop, ed., Academic Press, San Diego, (1994), and Carillo, H., and Lipton, D., SIAM J Applied Math 48:1073 (1988).
- 20 Methods for aligning polynucleotides or polypeptides are codified in computer programs, including the GCG program package (Devereux, J., et al., Nucleic Acids Research (1984) 12(1):387 (1984)), BLASTP, BLASTN, FASTA (Atschul, S.F. et al., J. Molec. Biol. 215:403 (1990), Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park,
- 25 35 575 Science Drive, Madison, WI 53711 (using the local homology algorithm of Smith and Waterman, Advances in Applied Mathematics 2:482-489 (1981)).

When using any of the sequence alignment programs to determine whether a particular sequence is, for instance, 95% identical to a reference sequence, the parameters are set so that the percentage of identity is calculated over the full length of the reference polynucleotide and that gaps in identity of up to 5% of the total number of nucleotides in the reference polynucleotide are allowed.

- 5 A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. 6:237-245 10 (1990).) The term "sequence" includes nucleotide and amino acid sequences. In a sequence alignment the query and subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB search of a DNA sequence to calculate percent identiy are: Matrix=Unitary, k-tuple=4, Mismatch 15 Penalty=1, Joining Penalty=30, Randomization Group Length=0, and Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, and Window Size=500 or query sequence length in nucleotide bases, whichever is shorter. Preferred parameters employed to calculate percent identity and similarity of an amino acid alignment are: Matrix=PAM 150, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group 20 Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty=0.05, and Window Size=500 or query sequence length in amino acid residues, whichever is shorter.

As an illustration, a polynucleotide having a nucleotide sequence of at least 95% "identity" to a sequence contained in SEQ ID NO:X or the cDNA contained in the deposited clone, means that the polynucleotide is identical to a sequence contained in 25 SEQ ID NO:X or the cDNA except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the total length (not just within a given 100 nucleotide stretch). In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to SEQ ID NO:X or the deposited clone, up to 5% of the nucleotides in the sequence contained in SEQ ID NO:X or the cDNA can be deleted, 30 inserted, or substituted with other nucleotides. These changes may occur anywhere throughout the polynucleotide.

Further embodiments of the present invention include polynucleotides having at least 85% identity, more preferably at least 90% identity, and most preferably at least 95%, 96%, 97%, 98% or 99% identity to a sequence contained in SEQ ID NO:X or the 35 cDNA contained in the deposited clone. Of course, due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the polynucleotides having at least 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity

will encode a polypeptide identical to an amino acid sequence contained in SEQ ID NO:Y or the expressed protein produced by the deposited clone.

- Similarly, by a polypeptide having an amino acid sequence having at least, for example, 95% "identity" to a reference polypeptide, is intended that the amino acid sequence of the polypeptide is identical to the reference polypeptide except that the polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the total length of the reference polypeptide. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a reference amino acid sequence, up to 5% of the amino acid residues in the reference sequence may be deleted or substituted with another amino acid, or a number of amino acids up to 5% of the total amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

- Further embodiments of the present invention include polypeptides having at least 80% identity, more preferably at least 85% identity, more preferably at least 90% identity, and most preferably at least 95%, 96%, 97%, 98% or 99% identity to an amino acid sequence contained in SEQ ID NO:Y or the expressed protein produced by the deposited clone. Preferably, the above polypeptides should exhibit at least one biological activity of the protein.

- In a preferred embodiment, polypeptides of the present invention include polypeptides having at least 90% similarity, more preferably at least 95% similarity, and still more preferably at least 96%, 97%, 98%, or 99% similarity to an amino acid sequence contained in SEQ ID NO:Y or the expressed protein produced by the deposited clone.

- The variants may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, variants in which 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host (change codons in the human mRNA to those preferred by a bacterial host such as *E. coli*).

Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an

organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985).) These allelic variants can vary at either the polynucleotide and/or polypeptide level. Alternatively, non-naturally occurring variants may be produced by mutagenesis techniques or by direct synthesis.

5       Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, one or more amino acids can be deleted from the N-terminus or C-terminus of the secreted protein without substantial loss of biological function. The authors of Ron et al., J. Biol. Chem. 268: 2984-2988  
10      10 (1993), reported variant KGF proteins having heparin binding activity even after deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the carboxy terminus of this protein. (Dobeli et al., J. Biotechnology 7:199-216 (1988).)

15      Moreover, ample evidence demonstrates that variants often retain a biological activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (J. Biol. Chem 268:22105-22111 (1993)) conducted extensive mutational analysis of human cytokine IL-1 $\alpha$ . They used random mutagenesis to generate over 3,500 individual IL-1 $\alpha$  mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible  
20      20 amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." (See, Abstract.) In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type.

25      Furthermore, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the secreted form will likely be retained when less than the majority of the residues of the secreted form  
30      30 are removed from the N-terminus or C-terminus. Whether a particular polypeptide lacking N- or C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

Thus, the invention further includes polypeptide variants which show  
35      35 substantial biological activity. Such variants include deletions, insertions, inversions, repeats, and substitutions selected according to general rules known in the art so as have little effect on activity. For example, guidance concerning how to make

phenotypically silent amino acid substitutions is provided in Bowie, J. U. et al., Science 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.

The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid substitution could be modified while still maintaining biological activity of the protein.

The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. (Cunningham and Wells, Science 244:1081-1085 (1989).) The resulting mutant molecules can then be tested for biological activity.

As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the protein. For example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly.

Besides conservative amino acid substitution, variants of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues, where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more of amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), or (iv) fusion of the polypeptide with additional amino acids, such as an IgG Fc fusion region peptide, or leader or secretory sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

- For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's
- 5 immunogenic activity. (Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

#### **Polynucleotide and Polypeptide Fragments**

- 10 In the present invention, a "polynucleotide fragment" refers to a short polynucleotide having a nucleic acid sequence contained in the deposited clone or shown in SEQ ID NO:X. The short nucleotide fragments are preferably at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length. A fragment "at least 20 nt in
- 15 length," for example, is intended to include 20 or more contiguous bases from the cDNA sequence contained in the deposited clone or the nucleotide sequence shown in SEQ ID NO:X. These nucleotide fragments are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments (e.g., 50, 150, 500, 600, 2000 nucleotides) are preferred.
- 20 Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments having a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 651-700, or 701 to the end of SEQ ID NO:X or the cDNA contained in the deposited clone. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has biological activity.

- In the present invention, a "polypeptide fragment" refers to a short amino acid sequence contained in SEQ ID NO:Y or encoded by the cDNA contained in the
- 30 deposited clone. Protein fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 102-120, 121-140, 141-160, or 161 to the end of the coding region. Moreover, polypeptide fragments can be about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about"

includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) amino acids, at either extreme or at both extremes.

- Preferred polypeptide fragments include the secreted protein as well as the mature form. Further preferred polypeptide fragments include the secreted protein or the mature form having a continuous series of deleted residues from the amino or the carboxy terminus, or both. For example, any number of amino acids, ranging from 1-60, can be deleted from the amino terminus of either the secreted polypeptide or the mature form. Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the secreted protein or mature form. Furthermore, any combination of the above amino and carboxy terminus deletions are preferred.
- Similarly, polynucleotide fragments encoding these polypeptide fragments are also preferred.

- Also preferred are polypeptide and polynucleotide fragments characterized by structural or functional domains, such as fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet-forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions, substrate binding region, and high antigenic index regions.
- Polypeptide fragments of SEQ ID NO:Y falling within conserved domains are specifically contemplated by the present invention. Moreover, polynucleotide fragments encoding these domains are also contemplated.

- Other preferred fragments are biologically active fragments. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

#### Epitopes & Antibodies

- In the present invention, "epitopes" refer to polypeptide fragments having antigenic or immunogenic activity in an animal, especially in a human. A preferred embodiment of the present invention relates to a polypeptide fragment comprising an epitope, as well as the polynucleotide encoding this fragment. A region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." In contrast, an "immunogenic epitope" is defined as a part of a protein that elicits an antibody response. (See, for instance, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998- 4002 (1983).)

Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985) further described in U.S. Patent No. 4,631,211.)

In the present invention, antigenic epitopes preferably contain a sequence of at least seven, more preferably at least nine, and most preferably between about 15 to about 30 amino acids. Antigenic epitopes are useful to raise antibodies, including monoclonal antibodies, that specifically bind the epitope. (See, for instance, Wilson et al., Cell 37:767-778 (1984); Sutcliffe, J. G. et al., Science 219:660-666 (1983).)

Similarly, immunogenic epitopes can be used to induce antibodies according to methods well known in the art. (See, for instance, Sutcliffe et al., *supra*; Wilson et al., *supra*; Chow, M. et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle, F. J. et al., J. Gen. Virol. 66:2347-2354 (1985).) A preferred immunogenic epitope includes the secreted protein. The immunogenic epitopes may be presented together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse) or, if it is long enough (at least about 25 amino acids), without a carrier. However, immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting.)

As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to include intact molecules as well as antibody fragments (such as, for example, Fab and F(ab')<sub>2</sub> fragments) which are capable of specifically binding to protein. Fab and F(ab')<sub>2</sub> fragments lack the Fc fragment of intact antibody, clear more rapidly from the circulation, and may have less non-specific tissue binding than an intact antibody. (Wahl et al., J. Nucl. Med. 24:316-325 (1983).) Thus, these fragments are preferred, as well as the products of a FAB or other immunoglobulin expression library. Moreover, antibodies of the present invention include chimeric, single chain, and humanized antibodies.

### Fusion Proteins

Any polypeptide of the present invention can be used to generate fusion proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because secreted proteins target cellular locations based on trafficking signals, the polypeptides of the present invention can be used as targeting molecules once fused to other proteins.

Examples of domains that can be fused to polypeptides of the present invention include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker sequences.

- 5 Moreover, fusion proteins may also be engineered to improve characteristics of the polypeptide of the present invention. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence during purification from the host cell or subsequent handling and storage. Also, peptide moieties may be added to the  
10 polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art.

- Moreover, polypeptides of the present invention, including fragments, and specifically epitopes, can be combined with parts of the constant domain of  
15 immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life in vivo. One reported example describes chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EP A 394,827; Traunecker et al., Nature 331:84-86  
20 (1988).) Fusion proteins having disulfide-linked dimeric structures (due to the IgG) can also be more efficient in binding and neutralizing other molecules, than the monomeric secreted protein or protein fragment alone. (Fountoulakis et al., J. Biochem. 270:3958-3964 (1995).)

- Similarly, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion  
25 proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP-A 0232 262.) Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified,  
30 would be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, D. Bennett et al., J. Molecular Recognition 8:52-58 (1995); K. Johanson et al., J. Biol.  
35 Chem. 270:9459-9471 (1995).)

Moreover, the polypeptides of the present invention can be fused to marker sequences, such as a peptide which facilitates purification of the fused polypeptide. In

preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for 5 instance, hexa-histidine provides for convenient purification of the fusion protein. Another peptide tag useful for purification, the "HA" tag, corresponds to an epitope derived from the influenza hemagglutinin protein. (Wilson et al., Cell 37:767 (1984).) Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the present invention.

10

#### Vectors, Host Cells, and Protein Production

The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral 15 vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is 20 a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp, phoA and tac 25 promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon at the beginning and a termination codon (UAA, UGA or 30 UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance genes for culturing in E. coli and other bacteria. Representative examples of 35 appropriate hosts include, but are not limited to, bacterial cells, such as E. coli, Streptomyces and Salmonella typhimurium cells; fungal cells, such as yeast cells; insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS,

293, and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A,

5 pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

10 Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., Basic Methods In Molecular Biology (1986). It is specifically contemplated that the polypeptides of the 15 present invention may in fact be expressed by a host cell lacking a recombinant vector.

A polypeptide of this invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity 20 chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

25 Polypeptides of the present invention, and preferably the secreted form, can also be recovered from: products purified from natural sources, including bodily fluids, tissues and cells, whether directly isolated or cultured; products of chemical synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be 30 non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the 35 translation initiation codon generally is removed with high efficiency from any protein after translation in all eukaryotic cells. While the N-terminal methionine on most proteins also is efficiently removed in most prokaryotes, for some proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

### Uses of the Polynucleotides

Each of the polynucleotides identified herein can be used in numerous ways as reagents. The following description should be considered exemplary and utilizes

5 known techniques.

The polynucleotides of the present invention are useful for chromosome identification. There exists an ongoing need to identify new chromosome markers, since few chromosome marking reagents, based on actual sequence data (repeat polymorphisms), are presently available. Each polynucleotide of the present invention  
10 can be used as a chromosome marker.

Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp) from the sequences shown in SEQ ID NO:X. Primers can be selected using computer analysis so that primers do not span more than one predicted exon in the genomic DNA. These primers are then used for PCR screening of somatic  
15 cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the SEQ ID NO:X will yield an amplified fragment.

Similarly, somatic hybrids provide a rapid method of PCR mapping the polynucleotides to particular chromosomes. Three or more clones can be assigned per day using a single thermal cycler. Moreover, sublocalization of the polynucleotides can  
20 be achieved with panels of specific chromosome fragments. Other gene mapping strategies that can be used include *in situ* hybridization, prescreening with labeled flow-sorted chromosomes, and preselection by hybridization to construct chromosome specific-cDNA libraries.

Precise chromosomal location of the polynucleotides can also be achieved using  
25 fluorescence *in situ* hybridization (FISH) of a metaphase chromosomal spread. This technique uses polynucleotides as short as 500 or 600 bases; however, polynucleotides 2,000-4,000 bp are preferred. For a review of this technique, see Verma et al., "Human Chromosomes: a Manual of Basic Techniques," Pergamon Press, New York (1988).

30 For chromosome mapping, the polynucleotides can be used individually (to mark a single chromosome or a single site on that chromosome) or in panels (for marking multiple sites and/or multiple chromosomes). Preferred polynucleotides correspond to the noncoding regions of the cDNAs because the coding sequences are more likely conserved within gene families, thus increasing the chance of cross  
35 hybridization during chromosomal mapping.

Once a polynucleotide has been mapped to a precise chromosomal location, the physical position of the polynucleotide can be used in linkage analysis. Linkage

analysis establishes coinheritance between a chromosomal location and presentation of a particular disease. (Disease mapping data are found, for example, in V. McKusick, Mendelian Inheritance in Man (available on line through Johns Hopkins University Welch Medical Library).) Assuming 1 megabase mapping resolution and one gene per

- 5 20 kb, a cDNA precisely localized to a chromosomal region associated with the disease could be one of 50-500 potential causative genes.

Thus, once coinheritance is established, differences in the polynucleotide and the corresponding gene between affected and unaffected individuals can be examined.

First, visible structural alterations in the chromosomes, such as deletions or

- 10 translocations, are examined in chromosome spreads or by PCR. If no structural alterations exist, the presence of point mutations are ascertained. Mutations observed in some or all affected individuals, but not in normal individuals, indicates that the mutation may cause the disease. However, complete sequencing of the polypeptide and the corresponding gene from several normal individuals is required to distinguish the 15 mutation from a polymorphism. If a new polymorphism is identified, this polymorphic polypeptide can be used for further linkage analysis.

Furthermore, increased or decreased expression of the gene in affected individuals as compared to unaffected individuals can be assessed using polynucleotides of the present invention. Any of these alterations (altered expression, 20 chromosomal rearrangement, or mutation) can be used as a diagnostic or prognostic marker.

In addition to the foregoing, a polynucleotide can be used to control gene expression through triple helix formation or antisense DNA or RNA. Both methods rely on binding of the polynucleotide to DNA or RNA. For these techniques, preferred 25 polynucleotides are usually 20 to 40 bases in length and complementary to either the region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxy-nucleotides as Antisense Inhibitors of Gene Expression, CRC

- 30 Press, Boca Raton, FL (1988).) Triple helix formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques are effective in model systems, and the information disclosed herein can be used to design antisense or triple helix polynucleotides in an effort to treat disease.

- 35 Polynucleotides of the present invention are also useful in gene therapy. One goal of gene therapy is to insert a normal gene into an organism having a defective gene, in an effort to correct the genetic defect. The polynucleotides disclosed in the

present invention offer a means of targeting such genetic defects in a highly accurate manner. Another goal is to insert a new gene that was not present in the host genome, thereby producing a new trait in the host cell.

The polynucleotides are also useful for identifying individuals from minute biological samples. The United States military, for example, is considering the use of restriction fragment length polymorphism (RFLP) for identification of its personnel. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identifying personnel. This method does not suffer from the current limitations of "Dog Tags" which can be lost, switched, or stolen, making positive identification difficult. The polynucleotides of the present invention can be used as additional DNA markers for RFLP.

The polynucleotides of the present invention can also be used as an alternative to RFLP, by determining the actual base-by-base DNA sequence of selected portions of an individual's genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, individuals can be identified because each individual will have a unique set of DNA sequences. Once an unique ID database is established for an individual, positive identification of that individual, living or dead, can be made from extremely small tissue samples.

Forensic biology also benefits from using DNA-based identification techniques as disclosed herein. DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, etc., can be amplified using PCR. In one prior art technique, gene sequences amplified from polymorphic loci, such as DQa class II HLA gene, are used in forensic biology to identify individuals. (Erlich, H., PCR Technology, Freeman and Co. (1992).) Once these specific polymorphic loci are amplified, they are digested with one or more restriction enzymes, yielding an identifying set of bands on a Southern blot probed with DNA corresponding to the DQa class II HLA gene. Similarly, polynucleotides of the present invention can be used as polymorphic markers for forensic purposes.

There is also a need for reagents capable of identifying the source of a particular tissue. Such need arises, for example, in forensics when presented with tissue of unknown origin. Appropriate reagents can comprise, for example, DNA probes or primers specific to particular tissue prepared from the sequences of the present invention. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

- In the very least, the polynucleotides of the present invention can be used as molecular weight markers on Southern gels, as diagnostic probes for the presence of a specific mRNA in a particular cell type, as a probe to "subtract-out" known sequences in the process of discovering novel polynucleotides, for selecting and making oligomers
- 5 for attachment to a "gene chip" or other support, to raise anti-DNA antibodies using DNA immunization techniques, and as an antigen to elicit an immune response.

### Uses of the Polypeptides

Each of the polypeptides identified herein can be used in numerous ways. The  
10 following description should be considered exemplary and utilizes known techniques.

A polypeptide of the present invention can be used to assay protein levels in a biological sample using antibody-based techniques. For example, protein expression in tissues can be studied with classical immunohistological methods. (Jalkanen, M., et al., J. Cell. Biol. 101:976-985 (1985); Jalkanen, M., et al., J. Cell. Biol. 105:3087-  
15 3096 (1987).) Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase, and radioisotopes, such as iodine (125I, 121I), carbon (14C), sulfur (35S), tritium (3H), indium (112In), and  
20 technetium (99mTc), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

In addition to assaying secreted protein levels in a biological sample, proteins can also be detected in vivo by imaging. Antibody labels or markers for in vivo imaging of protein include those detectable by X-radiography, NMR or ESR. For X-  
25 radiography, suitable labels include radioisotopes such as barium or cesium, which emit detectable radiation but are not overtly harmful to the subject. Suitable markers for NMR and ESR include those with a detectable characteristic spin, such as deuterium, which may be incorporated into the antibody by labeling of nutrients for the relevant hybridoma.

30 A protein-specific antibody or antibody fragment which has been labeled with an appropriate detectable imaging moiety, such as a radioisotope (for example, 131I, 112In, 99mTc), a radio-opaque substance, or a material detectable by nuclear magnetic resonance, is introduced (for example, parenterally, subcutaneously, or intraperitoneally) into the mammal. It will be understood in the art that the size of the  
35 subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20

millicuries of 99mTc. The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which contain the specific protein. In vivo tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments." (Chapter 13 in Tumor Imaging: The

- 5 Radiochemical Detection of Cancer, S.W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982).)

Thus, the invention provides a diagnostic method of a disorder, which involves (a) assaying the expression of a polypeptide of the present invention in cells or body fluid of an individual; (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of a disorder.

10 Moreover, polypeptides of the present invention can be used to treat disease. For example, patients can be administered a polypeptide of the present invention in an effort to replace absent or decreased levels of the polypeptide (e.g., insulin), to 15 supplement absent or decreased levels of a different polypeptide (e.g., hemoglobin S for hemoglobin B), to inhibit the activity of a polypeptide (e.g., an oncogene), to activate the activity of a polypeptide (e.g., by binding to a receptor), to reduce the activity of a membrane bound receptor by competing with it for free ligand (e.g., soluble TNF receptors used in reducing inflammation), or to bring about a desired 20 response (e.g., blood vessel growth).

Similarly, antibodies directed to a polypeptide of the present invention can also 25 be used to treat disease. For example, administration of an antibody directed to a polypeptide of the present invention can bind and reduce overproduction of the polypeptide. Similarly, administration of an antibody can activate the polypeptide, such as by binding to a polypeptide bound to a membrane (receptor).

At the very least, the polypeptides of the present invention can be used as 30 molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art. Polypeptides can also be used to raise antibodies, which in turn are used to measure protein expression from a recombinant cell, as a way of assessing transformation of the host cell. Moreover, the polypeptides of the present invention can be used to test the following biological activities.

### Biological Activities

35 The polynucleotides and polypeptides of the present invention can be used in assays to test for one or more biological activities. If these polynucleotides and polypeptides do exhibit activity in a particular assay, it is likely that these molecules

may be involved in the diseases associated with the biological activity. Thus, the polynucleotides and polypeptides could be used to treat the associated disease.

### Immune Activity

- 5        A polypeptide or polynucleotide of the present invention may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells. Immune cells develop through a process called hematopoiesis, producing myeloid (platelets, red blood cells, neutrophils, and macrophages) and lymphoid (B and T lymphocytes) cells
- 10      from pluripotent stem cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g., by chemotherapy or toxins), or infectious. Moreover, a polynucleotide or polypeptide of the present invention can be used as a marker or detector of a particular immune system disease or disorder.
- 15      A polynucleotide or polypeptide of the present invention may be useful in treating or detecting deficiencies or disorders of hematopoietic cells. A polypeptide or polynucleotide of the present invention could be used to increase differentiation and proliferation of hematopoietic cells, including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease in certain (or many) types hematopoietic
- 20      cells. Examples of immunologic deficiency syndromes include, but are not limited to: blood protein disorders (e.g. agammaglobulinemia, dysgammaglobulinemia), ataxia telangiectasia, common variable immunodeficiency, Digeorge Syndrome, HIV infection, HTLV-BLV infection, leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte bactericidal dysfunction, severe combined immunodeficiency (SCIDs), Wiskott-Aldrich Disorder, anemia, thrombocytopenia, or hemoglobinuria.
- 25      Moreover, a polypeptide or polynucleotide of the present invention could also be used to modulate hemostatic (the stopping of bleeding) or thrombolytic activity (clot formation). For example, by increasing hemostatic or thrombolytic activity, a polynucleotide or polypeptide of the present invention could be used to treat blood
- 30      coagulation disorders (e.g., afibrinogenemia, factor deficiencies), blood platelet disorders (e.g. thrombocytopenia), or wounds resulting from trauma, surgery, or other causes. Alternatively, a polynucleotide or polypeptide of the present invention that can decrease hemostatic or thrombolytic activity could be used to inhibit or dissolve clotting. These molecules could be important in the treatment of heart attacks
- 35      (infarction), strokes, or scarring.

A polynucleotide or polypeptide of the present invention may also be useful in treating or detecting autoimmune disorders. Many autoimmune disorders result from

inappropriate recognition of self as foreign material by immune cells. This inappropriate recognition results in an immune response leading to the destruction of the host tissue. Therefore, the administration of a polypeptide or polynucleotide of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing autoimmune disorders.

Examples of autoimmune disorders that can be treated or detected by the present invention include, but are not limited to: Addison's Disease, hemolytic anemia, antiphospholipid syndrome, rheumatoid arthritis, dermatitis, allergic encephalomyelitis, 10 glomerulonephritis, Goodpasture's Syndrome, Graves' Disease, Multiple Sclerosis, Myasthenia Gravis, Neuritis, Ophthalmia, Bullous Pemphigoid, Pemphigus, Polyendocrinopathies, Purpura, Reiter's Disease, Stiff-Man Syndrome, Autoimmune Thyroiditis, Systemic Lupus Erythematosus, Autoimmune Pulmonary Inflammation, Guillain-Barre Syndrome, insulin dependent diabetes mellitus, and autoimmune 15 inflammatory eye disease.

Similarly, allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems, may also be treated by a polypeptide or polynucleotide of the present invention. Moreover, these molecules can be used to treat anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompatibility.

20 A polynucleotide or polypeptide of the present invention may also be used to treat and/or prevent organ rejection or graft-versus-host disease (GVHD). Organ rejection occurs by host immune cell destruction of the transplanted tissue through an immune response. Similarly, an immune response is also involved in GVHD, but, in this case, the foreign transplanted immune cells destroy the host tissues. The 25 administration of a polypeptide or polynucleotide of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing organ rejection or GVHD.

Similarly, a polypeptide or polynucleotide of the present invention may also be used to modulate inflammation. For example, the polypeptide or polynucleotide may 30 inhibit the proliferation and differentiation of cells involved in an inflammatory response. These molecules can be used to treat inflammatory conditions, both chronic and acute conditions, including inflammation associated with infection (e.g., septic shock, sepsis, or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute 35 rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, or resulting from over production of cytokines (e.g., TNF or IL-1.)

### Hyperproliferative Disorders

A polypeptide or polynucleotide can be used to treat or detect hyperproliferative disorders, including neoplasms. A polypeptide or polynucleotide of the present

- 5 invention may inhibit the proliferation of the disorder through direct or indirect interactions. Alternatively, a polypeptide or polynucleotide of the present invention may proliferate other cells which can inhibit the hyperproliferative disorder.

For example, by increasing an immune response, particularly increasing antigenic qualities of the hyperproliferative disorder or by proliferating, differentiating, 10 or mobilizing T-cells, hyperproliferative disorders can be treated. This immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, decreasing an immune response may also be a method of treating hyperproliferative disorders, such as a chemotherapeutic agent.

15 Examples of hyperproliferative disorders that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but are not limited to neoplasms located in the: abdomen, bone, breast, digestive system, liver, pancreas, peritoneum, endocrine glands (adrenal, parathyroid, pituitary, testicles, ovary, thymus, thyroid), eye, head and neck, nervous (central and peripheral), lymphatic system, 20 pelvic, skin, soft tissue, spleen, thoracic, and urogenital.

Similarly, other hyperproliferative disorders can also be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of such hyperproliferative disorders include, but are not limited to: hypergammaglobulinemia, lymphoproliferative disorders, paraproteinemias, purpura, sarcoidosis, Sezary 25 Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease, besides neoplasia, located in an organ system listed above.

### Infectious Disease

30 A polypeptide or polynucleotide of the present invention can be used to treat or detect infectious agents. For example, by increasing the immune response, particularly increasing the proliferation and differentiation of B and/or T cells, infectious diseases may be treated. The immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, the 35 polypeptide or polynucleotide of the present invention may also directly inhibit the infectious agent, without necessarily eliciting an immune response.

- Viruses are one example of an infectious agent that can cause disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of viruses, include, but are not limited to the following DNA and RNA viral families: Arbovirus, Adenoviridae, Arenaviridae, Arterivirus,  
5 Birnaviridae, Bunyaviridae, Caliciviridae, Circoviridae, Coronaviridae, Flaviviridae, Hepadnaviridae (Hepatitis), Herpesviridae (such as, Cytomegalovirus, Herpes Simplex, Herpes Zoster), Mononegavirus (e.g., Paramyxoviridae, Morbillivirus, Rhabdoviridae), Orthomyxoviridae (e.g., Influenza), Papovaviridae, Parvoviridae, Picornaviridae, Poxviridae (such as Smallpox or Vaccinia), Reoviridae (e.g.,  
10 Rotavirus), Retroviridae (HTLV-I, HTLV-II, Lentivirus), and Togaviridae (e.g., Rubivirus). Viruses falling within these families can cause a variety of diseases or symptoms, including, but not limited to: arthritis, bronchiolitis, encephalitis, eye infections (e.g., conjunctivitis, keratitis), chronic fatigue syndrome, hepatitis (A, B, C, E, Chronic Active, Delta), meningitis, opportunistic infections (e.g., AIDS),  
15 pneumonia, Burkitt's Lymphoma, chickenpox , hemorrhagic fever, Measles, Mumps, Parainfluenza, Rabies, the common cold, Polio, leukemia, Rubella, sexually transmitted diseases, skin diseases (e.g., Kaposi's, warts), and viremia. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.  
20 Similarly, bacterial or fungal agents that can cause disease or symptoms and that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following Gram-Negative and Gram-positive bacterial families and fungi: Actinomycetales (e.g., Corynebacterium, Mycobacterium, Nocardia), Aspergillosis, Bacillaceae (e.g., Anthrax, Clostridium), Bacteroidaceae,  
25 Blastomycosis, Bordetella, Borrelia, Brucellosis, Candidiasis, Campylobacter, Coccidioidomycosis, Cryptococcosis, Dermatocytoses, Enterobacteriaceae (Klebsiella, Salmonella, Serratia, Yersinia), Erysipelothonix, Helicobacter, Legionellosis, Leptospirosis, Listeria, Mycoplasmatales, Neisseriaceae (e.g., Acinetobacter, Gonorrhea, Menigococcal), Pasteurellacea Infections (e.g., Actinobacillus,  
30 Heamophilus, Pasteurella), Pseudomonas, Rickettsiaceae, Chlamydiaceae, Syphilis, and Staphylococcal. These bacterial or fungal families can cause the following diseases or symptoms, including, but not limited to: bacteremia, endocarditis, eye infections (conjunctivitis, tuberculosis, uveitis), gingivitis, opportunistic infections (e.g., AIDS related infections), paronychia, prosthesis-related infections, Reiter's Disease,  
35 respiratory tract infections, such as Whooping Cough or Empyema, sepsis, Lyme Disease, Cat-Scratch Disease, Dysentery, Paratyphoid Fever, food poisoning, Typhoid, pneumonia, Gonorrhea, meningitis, Chlamydia, Syphilis, Diphtheria,

Leprosy, Paratuberculosis, Tuberculosis, Lupus, Botulism, gangrene, tetanus, impetigo, Rheumatic Fever, Scarlet Fever, sexually transmitted diseases, skin diseases (e.g., cellulitis, dermatocycoses), toxemia, urinary tract infections, wound infections. A polypeptide or polynucleotide of the present invention can be used to treat or detect

5 any of these symptoms or diseases.

Moreover, parasitic agents causing disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following families: Amebiasis, Babesiosis, Coccidiosis, Cryptosporidiosis, Dientamoebiasis, Dourine, Ectoparasitic, Giardiasis, Helminthiasis, Leishmaniasis, Theileriasis, Toxoplasmosis, Trypanosomiasis, and Trichomonas.

10 These parasites can cause a variety of diseases or symptoms, including, but not limited to: Scabies, Trombiculiasis, eye infections, intestinal disease (e.g., dysentery, giardiasis), liver disease, lung disease, opportunistic infections (e.g., AIDS related), Malaria, pregnancy complications, and toxoplasmosis. A polypeptide or polynucleotide

15 of the present invention can be used to treat or detect any of these symptoms or diseases.

Preferably, treatment using a polypeptide or polynucleotide of the present invention could either be by administering an effective amount of a polypeptide to the patient, or by removing cells from the patient, supplying the cells with a polynucleotide

20 of the present invention, and returning the engineered cells to the patient (ex vivo therapy). Moreover, the polypeptide or polynucleotide of the present invention can be used as an antigen in a vaccine to raise an immune response against infectious disease.

### Regeneration

25 A polynucleotide or polypeptide of the present invention can be used to differentiate, proliferate, and attract cells, leading to the regeneration of tissues. (See, Science 276:59-87 (1997).) The regeneration of tissues could be used to repair, replace, or protect tissue damaged by congenital defects, trauma (wounds, burns, incisions, or ulcers), age, disease (e.g. osteoporosis, osteoarthritis, periodontal

30 disease, liver failure), surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, or systemic cytokine damage.

Tissues that could be regenerated using the present invention include organs (e.g., pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac), vascular (including vascular endothelium), nervous, hematopoietic, and

35 skeletal (bone, cartilage, tendon, and ligament) tissue. Preferably, regeneration occurs without or decreased scarring. Regeneration also may include angiogenesis.

Moreover, a polynucleotide or polypeptide of the present invention may increase regeneration of tissues difficult to heal. For example, increased tendon/ligament regeneration would quicken recovery time after damage. A polynucleotide or polypeptide of the present invention could also be used prophylactically in an effort to

5 avoid damage. Specific diseases that could be treated include of tendinitis, carpal tunnel syndrome, and other tendon or ligament defects. A further example of tissue regeneration of non-healing wounds includes pressure ulcers, ulcers associated with vascular insufficiency, surgical, and traumatic wounds.

Similarly, nerve and brain tissue could also be regenerated by using a

10 polynucleotide or polypeptide of the present invention to proliferate and differentiate nerve cells. Diseases that could be treated using this method include central and peripheral nervous system diseases, neuropathies, or mechanical and traumatic disorders (e.g., spinal cord disorders, head trauma, cerebrovascular disease, and stroke). Specifically, diseases associated with peripheral nerve injuries, peripheral

15 neuropathy (e.g., resulting from chemotherapy or other medical therapies), localized neuropathies, and central nervous system diseases (e.g., Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome), could all be treated using the polynucleotide or polypeptide of the present invention.

20

### Chemotaxis

A polynucleotide or polypeptide of the present invention may have chemotaxis activity. A chemotactic molecule attracts or mobilizes cells (e.g., monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells) to a particular site in the body, such as inflammation, infection, or site of hyperproliferation. The mobilized cells can then fight off and/or heal the particular trauma or abnormality.

A polynucleotide or polypeptide of the present invention may increase chemotactic activity of particular cells. These chemotactic molecules can then be used to

30 treat inflammation, infection, hyperproliferative disorders, or any immune system disorder by increasing the number of cells targeted to a particular location in the body. For example, chemotactic molecules can be used to treat wounds and other trauma to tissues by attracting immune cells to the injured location. Chemotactic molecules of the present invention can also attract fibroblasts, which can be used to treat wounds.

35 It is also contemplated that a polynucleotide or polypeptide of the present invention may inhibit chemotactic activity. These molecules could also be used to treat

disorders. Thus, a polynucleotide or polypeptide of the present invention could be used as an inhibitor of chemotaxis.

### **Binding Activity**

5 A polypeptide of the present invention may be used to screen for molecules that bind to the polypeptide or for molecules to which the polypeptide binds. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit (antagonist), or decrease activity of the polypeptide or the molecule bound. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or  
10 small molecules.

Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a fragment of the ligand, or a natural substrate, a ligand, a structural or functional mimetic. (See, Coligan et al., Current Protocols in Immunology 1(2):Chapter 5 (1991).) Similarly, the molecule can be closely related to the natural  
15 receptor to which the polypeptide binds, or at least, a fragment of the receptor capable of being bound by the polypeptide (e.g., active site). In either case, the molecule can be rationally designed using known techniques.

Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide, either as a secreted protein or on the cell  
20 membrane. Preferred cells include cells from mammals, yeast, Drosophila, or *E. coli*. Cells expressing the polypeptide (or cell membrane containing the expressed polypeptide) are then preferably contacted with a test compound potentially containing the molecule to observe binding, stimulation, or inhibition of activity of either the polypeptide or the molecule.

25 The assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a label, or in an assay involving competition with a labeled competitor. Further, the assay may test whether the candidate compound results in a signal generated by binding to the polypeptide.

Alternatively, the assay can be carried out using cell-free preparations,  
30 polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

35 Preferably, an ELISA assay can measure polypeptide level or activity in a sample (e.g., biological sample) using a monoclonal or polyclonal antibody. The

antibody can measure polypeptide level or activity by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

- All of these above assays can be used as diagnostic or prognostic markers. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptide from suitably manipulated cells or tissues.

- Therefore, the invention includes a method of identifying compounds which bind to a polypeptide of the invention comprising the steps of: (a) incubating a candidate binding compound with a polypeptide of the invention; and (b) determining if binding has occurred. Moreover, the invention includes a method of identifying agonists/antagonists comprising the steps of: (a) incubating a candidate compound with a polypeptide of the invention, (b) assaying a biological activity , and (b) determining if a biological activity of the polypeptide has been altered.

15

#### Other Activities

- A polypeptide or polynucleotide of the present invention may also increase or decrease the differentiation or proliferation of embryonic stem cells, besides, as discussed above, hematopoietic lineage.
- 20 A polypeptide or polynucleotide of the present invention may also be used to modulate mammalian characteristics, such as body height, weight, hair color, eye color, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery). Similarly, a polypeptide or polynucleotide of the present invention may be used to modulate mammalian metabolism affecting catabolism, anabolism, processing, utilization, and storage of energy.

- 25 A polypeptide or polynucleotide of the present invention may be used to change a mammal's mental state or physical state by influencing biorhythms, caricadic rhythms, depression (including depressive disorders), tendency for violence, tolerance for pain, reproductive capabilities (preferably by Activin or Inhibin-like activity), hormonal or endocrine levels, appetite, libido, memory, stress, or other cognitive qualities.

- 30 A polypeptide or polynucleotide of the present invention may also be used as a food additive or preservative, such as to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components.

**Other Preferred Embodiments**

Other preferred embodiments of the claimed invention include an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 50 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Clone Sequence and ending with the nucleotide at about the position of the 3'

10 Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Start Codon and ending with the nucleotide at about the position of the 3' Nucleotide of

15 the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Similarly preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 150 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

25 Further preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 500 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

A further preferred embodiment is a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ 30 ID NO:X beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

A further preferred embodiment is an isolated nucleic acid molecule comprising 35 a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence of SEQ ID NO:X.

Also preferred is an isolated nucleic acid molecule which hybridizes under stringent hybridization conditions to a nucleic acid molecule, wherein said nucleic acid molecule which hybridizes does not hybridize under stringent hybridization conditions to a nucleic acid molecule having a nucleotide sequence consisting of only A residues or  
5 of only T residues.

Also preferred is a composition of matter comprising a DNA molecule which comprises a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the material deposited with the American Type Culture Collection and given the ATCC Deposit Number shown in Table 1 for said  
10 cDNA Clone Identifier.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in the nucleotide sequence of a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the deposit given the  
15 ATCC Deposit Number shown in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said sequence of at least 50 contiguous nucleotides is included in the nucleotide sequence of the complete open reading frame sequence encoded by said human cDNA clone.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 150 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.  
20

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 500 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.  
25

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is a method for detecting in a biological sample a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical  
30 to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method  
35 comprises a step of comparing a nucleotide sequence of at least one nucleic acid molecule in said sample with a sequence selected from said group and determining

whether the sequence of said nucleic acid molecule in said sample is at least 95% identical to said selected sequence.

Also preferred is the above method wherein said step of comparing sequences comprises determining the extent of nucleic acid hybridization between nucleic acid

5 molecules in said sample and a nucleic acid molecule comprising said sequence selected from said group. Similarly, also preferred is the above method wherein said step of comparing sequences is performed by comparing the nucleotide sequence determined from a nucleic acid molecule in said sample with said sequence selected from said group. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

10 A further preferred embodiment is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting nucleic acid molecules in said sample, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

15 The method for identifying the species, tissue or cell type of a biological sample can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

20 Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject nucleic acid molecules, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

25 The method for diagnosing a pathological condition can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

- Also preferred is a composition of matter comprising isolated nucleic acid molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence
- 5 selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The nucleic acid molecules can comprise DNA molecules or RNA molecules.
- 10 Also preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1.
- Also preferred is a polypeptide, wherein said sequence of contiguous amino acids is included in the amino acid sequence of SEQ ID NO:Y in the range of positions
- 15 beginning with the residue at about the position of the First Amino Acid of the Secreted Portion and ending with the residue at about the Last Amino Acid of the Open Reading Frame as set forth for SEQ ID NO:Y in Table 1.
- Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the
- 20 amino acid sequence of SEQ ID NO:Y.
- Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.
- Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the complete amino acid sequence of SEQ ID NO:Y.
- Further preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the
- 30 ATCC Deposit Number shown for said cDNA clone in Table 1.
- Also preferred is a polypeptide wherein said sequence of contiguous amino acids is included in the amino acid sequence of a secreted portion of the secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in
- 35 Table 1.
- Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the

amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

- Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

- Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

- Further preferred is an isolated antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

- Further preferred is a method for detecting in a biological sample a polypeptide comprising an amino acid sequence which is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group and determining whether the sequence of said polypeptide molecule in said sample is at least 90% identical to said sequence of at least 10 contiguous amino acids.

- Also preferred is the above method wherein said step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group comprises determining the extent of specific binding of polypeptides in said sample to an antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an

amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

- 5 Also preferred is the above method wherein said step of comparing sequences is performed by comparing the amino acid sequence determined from a polypeptide molecule in said sample with said sequence selected from said group.

Also preferred is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting polypeptide molecules in  
10 said sample, if any, comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained  
15 in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method for identifying the species, tissue or cell type of a biological sample, which method comprises a step of detecting polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a  
20 sequence of at least 10 contiguous amino acids in a sequence selected from the above group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample  
25 obtained from said subject polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid  
30 sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

In any of these methods, the step of detecting said polypeptide molecules includes using an antibody.

35 Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a nucleotide sequence encoding a polypeptide wherein said polypeptide comprises an amino acid sequence that is at least

90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table

- 5 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said nucleotide sequence encoding a polypeptide has been optimized for expression of said polypeptide in a prokaryotic host.

- 10 Also preferred is an isolated nucleic acid molecule, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the  
15 ATCC Deposit Number shown for said cDNA clone in Table 1.

- 20 Further preferred is a method of making a recombinant vector comprising inserting any of the above isolated nucleic acid molecule into a vector. Also preferred is the recombinant vector produced by this method. Also preferred is a method of making a recombinant host cell comprising introducing the vector into a host cell, as well as the recombinant host cell produced by this method.

- 25 Also preferred is a method of making an isolated polypeptide comprising culturing this recombinant host cell under conditions such that said polypeptide is expressed and recovering said polypeptide. Also preferred is this method of making an isolated polypeptide, wherein said recombinant host cell is a eukaryotic cell and said polypeptide is a secreted portion of a human secreted protein comprising an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y beginning with the residue at the position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y wherein Y is an integer set forth in Table 1 and said position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y is defined in Table 1;  
30 and an amino acid sequence of a secreted portion of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The isolated polypeptide produced by this method is also preferred.

- 35 Also preferred is a method of treatment of an individual in need of an increased level of a secreted protein activity, which method comprises administering to such an individual a pharmaceutical composition comprising an amount of an isolated

polypeptide, polynucleotide, or antibody of the claimed invention effective to increase the level of said protein activity in said individual.

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of illustration and are not intended as limiting.

### Examples

#### Example 1: Isolation of a Selected cDNA Clone From the Deposited Sample

10        Each cDNA clone in a cited ATCC deposit is contained in a plasmid vector. Table 1 identifies the vectors used to construct the cDNA library from which each clone was isolated. In many cases, the vector used to construct the library is a phage vector from which a plasmid has been excised. The table immediately below correlates the 15 related plasmid for each phage vector used in constructing the cDNA library. For example, where a particular clone is identified in Table 1 as being isolated in the vector "Lambda Zap," the corresponding deposited clone is in "pBluescript."

	<u>Vector Used to Construct Library</u>	<u>Corresponding Deposited Plasmid</u>
	Lambda Zap	pBluescript (pBS)
20	Uni-Zap XR	pBluescript (pBS)
	Zap Express	pBK
	lafmid BA	plafmid BA
	pSport1	pSport1
	pCMVSport 2.0	pCMVSport 2.0
25	pCMVSport 3.0	pCMVSport 3.0
	pCR®2.1	pCR®2.1

20        Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128,256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., Nucleic Acids Res. 16:7583-7600 (1988); Alting-Mees, M. A. and Short, J. M., Nucleic Acids Res. 17:9494 (1989)) and pBK (Alting-Mees, M. A. et al., Strategies 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Both can be transformed into E. coli strain XL-1 Blue, also available from Stratagene. pBS comes in 4 forms SK+, SK-, KS+ and KS. The S and K refers to the orientation of the polylinker to the T7 and T3 primer sequences which flank the polylinker region ("S" is for SacI and "K" is for KpnI which

are the first sites on each respective end of the linker). "+" or "-" refer to the orientation of the f1 origin of replication ("ori"), such that in one orientation, single stranded rescue initiated from the f1 ori generates sense strand DNA and in the other, antisense.

- Vectors pSport1, pCMVSport 2.0 and pCMVSport 3.0, were obtained from
- 5 Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into E. coli strain DH10B, also available from Life Technologies. (See, for instance, Gruber, C. E., et al., Focus 15:59 (1993).) Vector lafmid BA (Bento Soares, Columbia University, NY) contains an ampicillin resistance gene and can be transformed into E. coli strain XL-1
- 10 Blue. Vector pCR<sup>®</sup>2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into E. coli strain DH10B, available from Life Technologies. (See, for instance, Clark, J. M., Nuc. Acids Res. 16:9677-9686 (1988) and Mead, D. et al., Bio/Technology 9: (1991).) Preferably, a polynucleotide of the present invention does not comprise the
- 15 phage vector sequences identified for the particular clone in Table 1, as well as the corresponding plasmid vector sequences designated above.

The deposited material in the sample assigned the ATCC Deposit Number cited in Table 1 for any given cDNA clone also may contain one or more additional plasmids, each comprising a cDNA clone different from that given clone. Thus, deposits sharing

20 the same ATCC Deposit Number contain at least a plasmid for each cDNA clone identified in Table 1. Typically, each ATCC deposit sample cited in Table 1 comprises a mixture of approximately equal amounts (by weight) of about 50 plasmid DNAs, each containing a different cDNA clone; but such a deposit sample may include plasmids for more or less than 50 cDNA clones, up to about 500 cDNA clones.

25 Two approaches can be used to isolate a particular clone from the deposited sample of plasmid DNAs cited for that clone in Table 1. First, a plasmid is directly isolated by screening the clones using a polynucleotide probe corresponding to SEQ ID NO:X.

Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized

30 using an Applied Biosystems DNA synthesizer according to the sequence reported. The oligonucleotide is labeled, for instance, with <sup>32</sup>P-γ-ATP using T4 polynucleotide kinase and purified according to routine methods. (E.g., Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982).) The plasmid mixture is transformed into a suitable host, as indicated above (such as

35 XL-1 Blue (Stratagene)) using techniques known to those of skill in the art, such as those provided by the vector supplier or in related publications or patents cited above.

The transformants are plated on 1.5% agar plates (containing the appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening (e.g., Sambrook et al., Molecular Cloning: A Laboratory

- 5 Manual, 2nd Edit., (1989), Cold Spring Harbor Laboratory Press, pages 1.93 to 1.104), or other techniques known to those of skill in the art.

Alternatively, two primers of 17-20 nucleotides derived from both ends of the SEQ ID NO:X (i.e., within the region of SEQ ID NO:X bounded by the 5' NT and the 3' NT of the clone defined in Table 1) are synthesized and used to amplify the desired 10 cDNA using the deposited cDNA plasmid as a template. The polymerase chain reaction is carried out under routine conditions, for instance, in 25 µl of reaction mixture with 0.5 ug of the above cDNA template. A convenient reaction mixture is 1.5-5 mM MgCl<sub>2</sub>, 0.01% (w/v) gelatin, 20 µM each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation 15 at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

20 Several methods are available for the identification of the 5' or 3' non-coding portions of a gene which may not be present in the deposited clone. These methods include but are not limited to, filter probing, clone enrichment using specific probes, and protocols similar or identical to 5' and 3' "RACE" protocols which are well known in the art. For instance, a method similar to 5' RACE is available for generating the 25 missing 5' end of a desired full-length transcript. (Fromont-Racine et al., Nucleic Acids Res. 21(7):1683-1684 (1993).)

Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcripts. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to 30 a known sequence of the gene of interest is used to PCR amplify the 5' portion of the desired full-length gene. This amplified product may then be sequenced and used to generate the full length gene.

This above method starts with total RNA isolated from the desired source, although poly-A+ RNA can be used. The RNA preparation can then be treated with 35 phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase should then

be inactivated and the RNA treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase.

- 5        This modified RNA preparation is used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction is used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that  
10      the 5' end sequence belongs to the desired gene.

**Example 2: Isolation of Genomic Clones Corresponding to a Polynucleotide**

A human genomic P1 library (Genomic Systems, Inc.) is screened by PCR  
15      using primers selected for the cDNA sequence corresponding to SEQ ID NO:X., according to the method described in Example 1. (See also, Sambrook.)

**Example 3: Tissue Distribution of Polypeptide**

Tissue distribution of mRNA expression of polynucleotides of the present  
20      invention is determined using protocols for Northern blot analysis, described by, among others, Sambrook et al. For example, a cDNA probe produced by the method described in Example 1 is labeled with P<sup>32</sup> using the rediprime™ DNA labeling system (Amersham Life Science), according to manufacturer's instructions. After labeling, the probe is purified using CHROMA SPIN-100™ column (Clontech Laboratories, Inc.),  
25      according to manufacturer's protocol number PT1200-1. The purified labeled probe is then used to examine various human tissues for mRNA expression.

Multiple Tissue Northern (MTN) blots containing various human tissues (H) or human immune system tissues (IM) (Clontech) are examined with the labeled probe using ExpressHyb™ hybridization solution (Clontech) according to manufacturer's  
30      protocol number PT1190-1. Following hybridization and washing, the blots are mounted and exposed to film at -70°C overnight, and the films developed according to standard procedures.

**Example 4: Chromosomal Mapping of the Polynucleotides**

35      An oligonucleotide primer set is designed according to the sequence at the 5' end of SEQ ID NO:X. This primer preferably spans about 100 nucleotides. This

primer set is then used in a polymerase chain reaction under the following set of conditions : 30 seconds, 95°C; 1 minute, 56°C; 1 minute, 70°C. This cycle is repeated 32 times followed by one 5 minute cycle at 70°C. Human, mouse, and hamster DNA is used as template in addition to a somatic cell hybrid panel containing individual 5 chromosomes or chromosome fragments (Bios, Inc). The reactions is analyzed on either 8% polyacrylamide gels or 3.5 % agarose gels. Chromosome mapping is determined by the presence of an approximately 100 bp PCR fragment in the particular somatic cell hybrid.

10 **Example 5: Bacterial Expression of a Polypeptide**

A polynucleotide encoding a polypeptide of the present invention is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence, as outlined in Example 1, to synthesize insertion fragments. The primers used to amplify the cDNA insert should preferably contain restriction sites, such as 15 BamHI and XbaI, at the 5' end of the primers in order to clone the amplified product into the expression vector. For example, BamHI and XbaI correspond to the restriction enzyme sites on the bacterial expression vector pQE-9. (Qiagen, Inc., Chatsworth, CA). This plasmid vector encodes antibiotic resistance (Amp<sup>r</sup>), a bacterial origin of replication (ori), an IPTG-regulatable promoter/operator (P/O), a ribosome binding site 20 (RBS), a 6-histidine tag (6-His), and restriction enzyme cloning sites.

The pQE-9 vector is digested with BamHI and XbaI and the amplified fragment is ligated into the pQE-9 vector maintaining the reading frame initiated at the bacterial RBS. The ligation mixture is then used to transform the E. coli strain M15/rep4 (Qiagen, Inc.) which contains multiple copies of the plasmid pREP4, which expresses 25 the lacI repressor and also confers kanamycin resistance (Kan<sup>r</sup>). Transformants are identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is isolated and confirmed by restriction analysis.

Clones containing the desired constructs are grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml). 30 The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The cells are grown to an optical density 600 (O.D.<sup>600</sup>) of between 0.4 and 0.6. IPTG (Isopropyl-B-D-thiogalacto pyranoside) is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression.

Cells are grown for an extra 3 to 4 hours. Cells are then harvested by centrifugation (20 mins at 6000Xg). The cell pellet is solubilized in the chaotropic agent 6 Molar Guanidine HCl by stirring for 3-4 hours at 4°C. The cell debris is removed by centrifugation, and the supernatant containing the polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (available from QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high affinity and can be purified in a simple one-step procedure (for details see: The QIAexpressionist (1995) QIAGEN, Inc., *supra*).

5 Briefly, the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, 10 the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the polypeptide is eluted with 6 M guanidine-HCl, pH 5.

10 The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the 15 protein can be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After 20 renaturation the proteins are eluted by the addition of 250 mM immidazole. Immidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein is stored at 4°C or frozen at -80°C.

In addition to the above expression vector, the present invention further includes 25 an expression vector comprising phage operator and promoter elements operatively linked to a polynucleotide of the present invention, called pHE4a. (ATCC Accession Number XXXXXX.) This vector contains: 1) a neomycinphosphotransferase gene as a selection marker, 2) an E. coli origin of replication, 3) a T5 phage promoter sequence, 4) two lac operator sequences, 5) a Shine-Delgarno sequence, and 6) the lactose operon repressor gene (lacIq). The origin of replication (oriC) is derived from pUC19 (LTI, Gaithersburg, MD). The promoter sequence and operator sequences are made 30 synthetically.

DNA can be inserted into the pHEa by restricting the vector with NdeI and XbaI, BamHI, XhoI, or Asp718, running the restricted product on a gel, and isolating the larger fragment (the stuffer fragment should be about 310 base pairs). The DNA insert is generated according to the PCR protocol described in Example 1, using PCR 35 primers having restriction sites for NdeI (5' primer) and XbaI, BamHI, XhoI, or

Asp718 (3' primer). The PCR insert is gel purified and restricted with compatible enzymes. The insert and vector are ligated according to standard protocols.

The engineered vector could easily be substituted in the above protocol to express protein in a bacterial system.

5

**Example 6: Purification of a Polypeptide from an Inclusion Body**

The following alternative method can be used to purify a polypeptide expressed in *E coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

- 10        Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.
- 15

- 15        The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 xg for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.
- 20

- 20        The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 xg centrifugation for 15 min., the pellet is discarded and the polypeptide containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.
- 25

- 25        Following high speed centrifugation (30,000 xg) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing 30 for 12 hours prior to further purification steps.

To clarify the refolded polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive

Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

- 5       Fractions containing the polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium  
10      acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant  $A_{280}$  monitoring of the effluent. Fractions containing the polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.  
15      The resultant polypeptide should exhibit greater than 95% purity after the above refolding and purification steps. No major contaminant bands should be observed from Commassie blue stained 16% SDS-PAGE gel when 5  $\mu$ g of purified protein is loaded. The purified protein can also be tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

20

**Example 7: Cloning and Expression of a Polypeptide in a Baculovirus Expression System**

In this example, the plasmid shuttle vector pA2 is used to insert a polynucleotide into a baculovirus to express a polypeptide. This expression vector contains the strong polyhedrin promoter of the *Autographa californica* nuclear polyhedrosis virus (AcMNPV) followed by convenient restriction sites such as BamHI, Xba I and Asp718. The polyadenylation site of the simian virus 40 ("SV40") is used for efficient polyadenylation. For easy selection of recombinant virus, the plasmid contains the beta-galactosidase gene from *E. coli* under control of a weak Drosophila promoter in the same orientation, followed by the polyadenylation signal of the polyhedrin gene. The inserted genes are flanked on both sides by viral sequences for cell-mediated homologous recombination with wild-type viral DNA to generate a viable virus that expresses the cloned polynucleotide.

Many other baculovirus vectors can be used in place of the vector above, such 35 as pAc373, pVL941, and pAcIM1, as one skilled in the art would readily appreciate, as long as the construct provides appropriately located signals for transcription,

translation, secretion and the like, including a signal peptide and an in-frame AUG as required. Such vectors are described, for instance, in Luckow et al., *Virology* 170:31-39 (1989).

- Specifically, the cDNA sequence contained in the deposited clone, including the
- 5 AUG initiation codon and the naturally associated leader sequence identified in Table 1, is amplified using the PCR protocol described in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the pA2 vector does not need a second signal peptide. Alternatively, the vector can be modified (pA2 GP) to include a baculovirus leader sequence, using the standard methods described in Summers et al.,
- 10 "A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures," Texas Agricultural Experimental Station Bulletin No. 1555 (1987).

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("Geneclean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

- 15 The plasmid is digested with the corresponding restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1% agarose gel using a commercially available kit ("Geneclean" BIO 101 Inc., La Jolla, Ca.).

- The fragment and the dephosphorylated plasmid are ligated together with T4  
20 DNA ligase. *E. coli* HB101 or other suitable *E. coli* hosts such as XL-1 Blue (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria containing the plasmid are identified by digesting DNA from individual colonies and analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA  
25 sequencing.

- Five µg of a plasmid containing the polynucleotide is co-transfected with 1.0 µg of a commercially available linearized baculovirus DNA ("BaculoGold™ baculovirus DNA", Pharmingen, San Diego, CA), using the lipofection method described by Felgner et al., *Proc. Natl. Acad. Sci. USA* 84:7413-7417 (1987). One µg of  
30 BaculoGold™ virus DNA and 5 µg of the plasmid are mixed in a sterile well of a microtiter plate containing 50 µl of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10 µl Lipofectin plus 90 µl Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm  
35 tissue culture plate with 1 ml Grace's medium without serum. The plate is then incubated for 5 hours at 27° C. The transfection solution is then removed from the plate

and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. Cultivation is then continued at 27° C for four days.

- After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, *supra*. An agarose gel with "Blue Gal" (Life Technologies Inc., Gaithersburg) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10.)
- 5 After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200 µl of Grace's medium and the suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then they are stored at 4° C.
- 10
- 15 To verify the expression of the polypeptide, Sf9 cells are grown in Grace's medium supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant baculovirus containing the polynucleotide at a multiplicity of infection ("MOI") of about 2. If radiolabeled proteins are desired, 6 hours later the medium is removed and is replaced with SF900 II medium minus methionine and cysteine.
- 20
- 25 (available from Life Technologies Inc., Rockville, MD). After 42 hours, 5 µCi of <sup>35</sup>S-methionine and 5 µCi <sup>35</sup>S-cysteine (available from Amersham) are added. The cells are further incubated for 16 hours and then are harvested by centrifugation. The proteins in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE followed by autoradiography (if radiolabeled).
- Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the produced protein.

#### **Example 8: Expression of a Polypeptide in Mammalian Cells**

The polypeptide of the present invention can be expressed in a mammalian cell. A typical mammalian expression vector contains a promoter element, which mediates the initiation of transcription of mRNA, a protein coding sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription is achieved with the early and late promoters from SV40, the long terminal repeats (LTRs) from Retroviruses, e.g., RSV, HTLV, HIVI and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter).

Suitable expression vectors for use in practicing the present invention include, for example, vectors such as pSVL and pMSG (Pharmacia, Uppsala, Sweden), pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146), pBC12MI (ATCC 67109), pCMVSport 2.0, and pCMVSport 3.0. Mammalian host cells that could be used 5 include, human Hela, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV1, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

Alternatively, the polypeptide can be expressed in stable cell lines containing the 10 polynucleotide integrated into a chromosome. The co-transfection with a selectable marker such as dhfr, gpt, neomycin, hygromycin allows the identification and isolation of the transfected cells.

The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful in developing 15 cell lines that carry several hundred or even several thousand copies of the gene of interest. (See, e.g., Alt, F. W., et al., J. Biol. Chem. 253:1357-1370 (1978); Hamlin, J. L. and Ma, C., Biochem. et Biophys. Acta, 1097:107-143 (1990); Page, M. J. and Sydenham, M. A., Biotechnology 9:64-68 (1991).) Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy et al., Biochem J. 227:277-279 (1991); Bebbington et al., Bio/Technology 10:169-175 (1992)). Using these markers, the 20 mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

Derivatives of the plasmid pSV2-dhfr (ATCC Accession No. 37146), the 25 expression vectors pC4 (ATCC Accession No. 209646) and pC6 (ATCC Accession No. 209647) contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen et al., Molecular and Cellular Biology, 438-447 (March, 1985)) plus a fragment of the CMV-enhancer (Boshart et al., Cell 41:521-530 (1985).) Multiple cloning sites, e.g., with the restriction enzyme cleavage sites BamHI, XbaI and Asp718, facilitate the 30 cloning of the gene of interest. The vectors also contain the 3' intron, the polyadenylation and termination signal of the rat preproinsulin gene, and the mouse DHFR gene under control of the SV40 early promoter.

Specifically, the plasmid pC6, for example, is digested with appropriate 35 restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel.

A polynucleotide of the present invention is amplified according to the protocol outlined in Example 1. If the naturally occurring signal sequence is used to produce the

secreted protein, the vector does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

5 The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("Geneclean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The amplified fragment is then digested with the same restriction enzyme and purified on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then 10 transformed and bacteria are identified that contain the fragment inserted into plasmid pC6 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene is used for transfection. Five  $\mu$ g of the expression plasmid pC6 is cotransfected with 0.5  $\mu$ g of the plasmid pSVneo using lipofectin (Felgner et al., *supra*). The plasmid pSV2-neo 15 contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. 20 After about 10-14 days single clones are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1  $\mu$ M, 2  $\mu$ M, 5  $\mu$ M, 10 mM, 20 mM). The same 25 procedure is repeated until clones are obtained which grow at a concentration of 100 - 200  $\mu$ M. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

#### Example 9: Protein Fusions

30 The polypeptides of the present invention are preferably fused to other proteins. These fusion proteins can be used for a variety of applications. For example, fusion of the present polypeptides to His-tag, HA-tag, protein A, IgG domains, and maltose binding protein facilitates purification. (See Example 5; see also EP A 394,827; Traunecker, et al., *Nature* 331:84-86 (1988).) Similarly, fusion to IgG-1, IgG-3, and 35 albumin increases the halflife time in vivo. Nuclear localization signals fused to the polypeptides of the present invention can target the protein to a specific subcellular localization, while covalent heterodimer or homodimers can increase or decrease the

activity of a fusion protein. Fusion proteins can also create chimeric molecules having more than one function. Finally, fusion proteins can increase solubility and/or stability of the fused protein compared to the non-fused protein. All of the types of fusion proteins described above can be made by modifying the following protocol, which

- 5 outlines the fusion of a polypeptide to an IgG molecule, or the protocol described in Example 5.

Briefly, the human Fc portion of the IgG molecule can be PCR amplified, using primers that span the 5' and 3' ends of the sequence described below. These primers also should have convenient restriction enzyme sites that will facilitate cloning into an

- 10 expression vector, preferably a mammalian expression vector.

For example, if pC4 (Accession No. 209646) is used, the human Fc portion can be ligated into the BamHI cloning site. Note that the 3' BamHI site should be destroyed. Next, the vector containing the human Fc portion is re-restricted with BamHI, linearizing the vector, and a polynucleotide of the present invention, isolated

- 15 by the PCR protocol described in Example 1, is ligated into this BamHI site. Note that the polynucleotide is cloned without a stop codon, otherwise a fusion protein will not be produced.

If the naturally occurring signal sequence is used to produce the secreted protein, pC4 does not need a second signal peptide. Alternatively, if the naturally

- 20 occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

Human IgG Fc region:

GGGATCCGGAGCCAAATCTTCTGACAAAACACACATGCCACC GTGCC  
25 CAGCACCTGAATTGAGGGTGACCGTCAGTCCTCTCCCCCAAAACC  
CAAGGACACCTCATGATCTCCGGACTCCTGAGGTACATGCGTGGTGGT  
GGACGTAAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACG  
GCGTGGAGGTGCATAATGCCAAGACAAAGCCGGGAGGAGCAGTACAAC  
AGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG  
30 AATGGCAAGGAGTACAAGTGCAGGTCTCCAACAAAGCCCTCCAACCCCC  
ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACACAGGT  
GTACACCCCTGCCCTCATCCGGATGAGCTGACCAAGAACCAAGGTCAGCCT  
GACCTGCCTGGTCAAAGGCTTCTATCCAAGCGACATGCCGTGGAGTGGGA  
GAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCGTGCTGG  
35 ACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA  
GGTGGCAGCAGGGAACGTCTCATGCTCCGTGATGCATGAGGCTCTGC

ACAACCACACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGTAAATGAGTGC  
GACGGCCGCGACTCTAGAGGAT (SEQ ID NO:1)

**Example 10: Production of an Antibody from a Polypeptide**

- 5       The antibodies of the present invention can be prepared by a variety of methods. (See, Current Protocols, Chapter 2.) For example, cells expressing a polypeptide of the present invention is administered to an animal to induce the production of sera containing polyclonal antibodies. In a preferred method, a preparation of the secreted protein is prepared and purified to render it substantially free of natural contaminants.
- 10      Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

In the most preferred method, the antibodies of the present invention are monoclonal antibodies (or protein binding fragments thereof). Such monoclonal antibodies can be prepared using hybridoma technology. (Köhler et al., *Nature* 256:495 (1975); Köhler et al., *Eur. J. Immunol.* 6:511 (1976); Köhler et al., *Eur. J. Immunol.* 6:292 (1976); Hammerling et al., in: *Monoclonal Antibodies and T-Cell Hybridomas*, Elsevier, N.Y., pp. 563-681 (1981).) In general, such procedures involve immunizing an animal (preferably a mouse) with polypeptide or, more preferably, with a secreted polypeptide-expressing cell. Such cells may be cultured in any suitable tissue culture medium; however, it is preferable to culture cells in Earle's modified Eagle's medium supplemented with 10% fetal bovine serum (inactivated at about 56°C), and supplemented with about 10 g/l of nonessential amino acids, about 1,000 U/ml of penicillin, and about 100 µg/ml of streptomycin.

The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands et al. (*Gastroenterology* 80:225-232 (1981).) The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the polypeptide.

Alternatively, additional antibodies capable of binding to the polypeptide can be produced in a two-step procedure using anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal, preferably a

mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the protein-specific antibody can be blocked by the polypeptide. Such antibodies comprise anti-idiotypic antibodies to the protein-specific antibody and

5 can be used to immunize an animal to induce formation of further protein-specific antibodies.

It will be appreciated that Fab and F(ab')2 and other fragments of the antibodies of the present invention may be used according to the methods disclosed herein. Such fragments are typically produced by proteolytic cleavage, using enzymes such as papain

10 (to produce Fab fragments) or pepsin (to produce F(ab')2 fragments). Alternatively, secreted protein-binding fragments can be produced through the application of recombinant DNA technology or through synthetic chemistry.

For in vivo use of antibodies in humans, it may be preferable to use "humanized" chimeric monoclonal antibodies. Such antibodies can be produced using

15 genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric antibodies are known in the art. (See, for review, Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO

20 8702671; Boulian et al., Nature 312:643 (1984); Neuberger et al., Nature 314:268 (1985).)

**Example 11: Production Of Secreted Protein For High-Throughput Screening Assays**

25 The following protocol produces a supernatant containing a polypeptide to be tested. This supernatant can then be used in the Screening Assays described in Examples 13-20.

First, dilute Poly-D-Lysine (644 587 Boehringer-Mannheim) stock solution (1mg/ml in PBS) 1:20 in PBS (w/o calcium or magnesium 17-516F Biowhittaker) for a

30 working solution of 50ug/ml. Add 200 ul of this solution to each well (24 well plates) and incubate at RT for 20 minutes. Be sure to distribute the solution over each well (note: a 12-channel pipetter may be used with tips on every other channel). Aspirate off the Poly-D-Lysine solution and rinse with 1ml PBS (Phosphate Buffered Saline). The PBS should remain in the well until just prior to plating the cells and plates may be

35 poly-lysine coated in advance for up to two weeks.

Plate 293T cells (do not carry cells past P+20) at  $2 \times 10^5$  cells/well in .5ml DMEM(Dulbecco's Modified Eagle Medium)(with 4.5 G/L glucose and L-glutamine

(12-604F Biowhittaker))/10% heat inactivated FBS(14-503F Biowhittaker)/1x Penstrep(17-602E Biowhittaker). Let the cells grow overnight.

The next day, mix together in a sterile solution basin: 300 ul Lipofectamine (18324-012 Gibco/BRL) and 5ml Optimem I (31985070 Gibco/BRL)/96-well plate.

- 5 With a small volume multi-channel pipetter, aliquot approximately 2ug of an expression vector containing a polynucleotide insert, produced by the methods described in Examples 8 or 9, into an appropriately labeled 96-well round bottom plate. With a multi-channel pipetter, add 50ul of the Lipofectamine/Optimem I mixture to each well. Pipette up and down gently to mix. Incubate at RT 15-45 minutes. After about 20
- 10 minutes, use a multi-channel pipetter to add 150ul Optimem I to each well. As a control, one plate of vector DNA lacking an insert should be transfected with each set of transfections.

Preferably, the transfection should be performed by tag-teaming the following tasks. By tag-teaming, hands on time is cut in half, and the cells do not spend too much time on PBS. First, person A aspirates off the media from four 24-well plates of cells, and then person B rinses each well with .5-1ml PBS. Person A then aspirates off PBS rinse, and person B, using a12-channel pipetter with tips on every other channel, adds the 200ul of DNA/Lipofectamine/Optimem I complex to the odd wells first, then to the even wells, to each row on the 24-well plates. Incubate at 37°C for 6 hours.

- 20 While cells are incubating, prepare appropriate media, either 1%BSA in DMEM with 1x penstrep, or CHO-5 media (116.6 mg/L of CaCl<sub>2</sub> (anhyd); 0.00130 mg/L CuSO<sub>4</sub>·5H<sub>2</sub>O; 0.050 mg/L of Fe(NO<sub>3</sub>)<sub>3</sub>·9H<sub>2</sub>O; 0.417 mg/L of FeSO<sub>4</sub>·7H<sub>2</sub>O; 311.80 mg/L of KCl; 28.64 mg/L of MgCl<sub>2</sub>; 48.84 mg/L of MgSO<sub>4</sub>; 6995.50 mg/L of NaCl; 2400.0 mg/L of NaHCO<sub>3</sub>; 62.50 mg/L of NaH<sub>2</sub>PO<sub>4</sub>·H<sub>2</sub>O; 71.02 mg/L of Na<sub>2</sub>HPO<sub>4</sub>; 25 .4320 mg/L of ZnSO<sub>4</sub>·7H<sub>2</sub>O; .002 mg/L of Arachidonic Acid ; 1.022 mg/L of Cholesterol; .070 mg/L of DL-alpha-Tocopherol-Acetate; 0.0520 mg/L of Linoleic Acid; 0.010 mg/L of Linolenic Acid; 0.010 mg/L of Myristic Acid; 0.010 mg/L of Oleic Acid; 0.010 mg/L of Palmitric Acid; 0.010 mg/L of Palmitic Acid; 100 mg/L of Pluronic F-68; 0.010 mg/L of Stearic Acid; 2.20 mg/L of Tween 80; 4551 mg/L of D-
- 30 Glucose; 130.85 mg/ml of L- Alanine; 147.50 mg/ml of L-Arginine-HCL; 7.50 mg/ml of L-Asparagine-H<sub>2</sub>O; 6.65 mg/ml of L-Aspartic Acid; 29.56 mg/ml of L-Cystine-2HCL-H<sub>2</sub>O; 31.29 mg/ml of L-Cystine-2HCL; 7.35 mg/ml of L-Glutamic Acid; 365.0 mg/ml of L-Glutamine; 18.75 mg/ml of Glycine; 52.48 mg/ml of L-Histidine-HCL-H<sub>2</sub>O; 106.97 mg/ml of L-Isoleucine; 111.45 mg/ml of L-Leucine; 163.75 mg/ml of L-
- 35 Lysine HCL; 32.34 mg/ml of L-Methionine; 68.48 mg/ml of L-Phenylalanine; 40.0 mg/ml of L-Proline; 26.25 mg/ml of L-Serine; 101.05 mg/ml of L-Threonine; 19.22

mg/ml of L-Tryptophan; 91.79 mg/ml of L-Tyrosine-2Na-2H<sub>2</sub>O; 99.65 mg/ml of L-Valine; 0.0035 mg/L of Biotin; 3.24 mg/L of D-Ca Pantothenate; 11.78 mg/L of Choline Chloride; 4.65 mg/L of Folic Acid; 15.60 mg/L of i-Inositol; 3.02 mg/L of Niacinamide; 3.00 mg/L of Pyridoxal HCL; 0.031 mg/L of Pyridoxine HCL; 0.319 mg/L of Riboflavin; 3.17 mg/L of Thiamine HCL; 0.365 mg/L of Thymidine; and 0.680 mg/L of Vitamin B<sub>12</sub>; 25 mM of HEPES Buffer; 2.39 mg/L of Na Hypoxanthine; 0.105 mg/L of Lipoic Acid; 0.081 mg/L of Sodium Putrescine-2HCL; 55.0 mg/L of Sodium Pyruvate; 0.0067 mg/L of Sodium Selenite; 20uM of Ethanolamine; 0.122 mg/L of Ferric Citrate; 41.70 mg/L of Methyl-B-Cyclodextrin complexed with Linoleic Acid; 33.33 mg/L of Methyl-B-Cyclodextrin complexed with Oleic Acid; and 10 mg/L of Methyl-B-Cyclodextrin complexed with Retinal) with 2mm glutamine and 1x penstrep. (BSA (81-068-3 Bayer) 100gm dissolved in 1L DMEM for a 10% BSA stock solution). Filter the media and collect 50 ul for endotoxin assay in 15ml polystyrene conical.

15       The transfection reaction is terminated, preferably by tag-teaming, at the end of the incubation period. Person A aspirates off the transfection media, while person B adds 1.5ml appropriate media to each well. Incubate at 37°C for 45 or 72 hours depending on the media used: 1%BSA for 45 hours or CHO-5 for 72 hours.

20       On day four, using a 300ul multichannel pipetter, aliquot 600ul in one 1ml deep well plate and the remaining supernatant into a 2ml deep well. The supernatants from each well can then be used in the assays described in Examples 13-20.

25       It is specifically understood that when activity is obtained in any of the assays described below using a supernatant, the activity originates from either the polypeptide directly (e.g., as a secreted protein) or by the polypeptide inducing expression of other proteins, which are then secreted into the supernatant. Thus, the invention further provides a method of identifying the protein in the supernatant characterized by an activity in a particular assay.

#### Example 12: Construction of GAS Reporter Construct

30       One signal transduction pathway involved in the differentiation and proliferation of cells is called the Jaks-STATs pathway. Activated proteins in the Jaks-STATs pathway bind to gamma activation site “GAS” elements or interferon-sensitive responsive element (“ISRE”), located in the promoter of many genes. The binding of a protein to these elements alter the expression of the associated gene.

35       GAS and ISRE elements are recognized by a class of transcription factors called Signal Transducers and Activators of Transcription, or “STATs.” There are six

- members of the STATs family. Stat1 and Stat3 are present in many cell types, as is Stat2 (as response to IFN-alpha is widespread). Stat4 is more restricted and is not in many cell types though it has been found in T helper class I, cells after treatment with IL-12. Stat5 was originally called mammary growth factor, but has been found at 5 higher concentrations in other cells including myeloid cells. It can be activated in tissue culture cells by many cytokines.

The STATs are activated to translocate from the cytoplasm to the nucleus upon tyrosine phosphorylation by a set of kinases known as the Janus Kinase ("Jaks") family. Jaks represent a distinct family of soluble tyrosine kinases and include Tyk2, 10 Jak1, Jak2, and Jak3. These kinases display significant sequence similarity and are generally catalytically inactive in resting cells.

The Jaks are activated by a wide range of receptors summarized in the Table below. (Adapted from review by Schidler and Darnell, Ann. Rev. Biochem. 64:621-51 1995.) A cytokine receptor family, capable of activating Jaks, is divided into two 15 groups: (a) Class 1 includes receptors for IL-2, IL-3, IL-4, IL-6, IL-7, IL-9, IL-11, IL-12, IL-15, Epo, PRL, GH, G-CSF, GM-CSF, LIF, CNTF, and thrombopoietin; and (b) Class 2 includes IFN- $\alpha$ , IFN- $\gamma$ , and IL-10. The Class 1 receptors share a 20 conserved cysteine motif (a set of four conserved cysteines and one tryptophan) and a WSXWS motif (a membrane proximal region encoding Trp-Ser-Xxx-Trp-Ser (SEQ ID NO:2)).

Thus, on binding of a ligand to a receptor, Jaks are activated, which in turn activate STATs, which then translocate and bind to GAS elements. This entire process is encompassed in the Jaks-STATs signal transduction pathway.

Therefore, activation of the Jaks-STATs pathway, reflected by the binding of 25 the GAS or the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells. For example, growth factors and cytokines are known to activate the Jaks-STATs pathway. (See Table below.) Thus, by using GAS elements linked to reporter molecules, activators of the Jaks-STATs pathway can be identified.



- To construct a synthetic GAS containing promoter element, which is used in the Biological Assays described in Examples 13-14, a PCR based strategy is employed to generate a GAS-SV40 promoter sequence. The 5' primer contains four tandem copies of the GAS binding site found in the IRF1 promoter and previously demonstrated to bind STATs upon induction with a range of cytokines (Rothman et al., *Immunity* 1:457-468 (1994).), although other GAS or ISRE elements can be used instead. The 5' primer also contains 18bp of sequence complementary to the SV40 early promoter sequence and is flanked with an XhoI site. The sequence of the 5' primer is:
- 5: GCGCCTCGAGATTCCCCGAAATCTAGATTCCCCGAAATGATTCCCCG  
10 AAATGATTCCCCGAAATATCTGCCATCTCAATTAG:3' (SEQ ID NO:3)
- The downstream primer is complementary to the SV40 promoter and is flanked with a Hind III site: 5': GCGGCAAGCTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)
- PCR amplification is performed using the SV40 promoter template present in the B-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI/Hind III and subcloned into BLSK2-. (Stratagene.) Sequencing with forward and reverse primers confirms that the insert contains the following sequence:
- 15 5': CTCGAGATTCCCCGAAATCTAGATTCCCCGAAATGATTCCCCGAAATG  
20 ATTTCCCCGAAATATCTGCCATCTCAATTAGTCAGCAACCATAGTCCGCC  
CTAACTCCGCCATCCGCCCTAACTCCGCCAGTTCCGCCATTCTCCGC  
CCCATGGCTGACTAATTTTTATTATGCAGAGGCCGAGGCCGCTCGGC  
CTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTGAGGCCTAGGCTTT  
TGCAAAAAGCTT:3' (SEQ ID NO:5)
- 25 With this GAS promoter element linked to the SV40 promoter, a GAS:SEAP2 reporter construct is next engineered. Here, the reporter molecule is a secreted alkaline phosphatase, or "SEAP." Clearly, however, any reporter molecule can be instead of SEAP, in this or in any of the other Examples. Well known reporter molecules that can be used instead of SEAP include chloramphenicol acetyltransferase (CAT), luciferase,
- 30 alkaline phosphatase, B-galactosidase, green fluorescent protein (GFP), or any protein detectable by an antibody.

The above sequence confirmed synthetic GAS-SV40 promoter element is subcloned into the pSEAP-Promoter vector obtained from Clontech using HindIII and XhoI, effectively replacing the SV40 promoter with the amplified GAS:SV40 promoter element, to create the GAS-SEAP vector. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

Thus, in order to generate mammalian stable cell lines expressing the GAS-SEAP reporter, the GAS-SEAP cassette is removed from the GAS-SEAP vector using SalI and NotI, and inserted into a backbone vector containing the neomycin resistance gene, such as pGFP-1 (Clontech), using these restriction sites in the multiple cloning site, to create the GAS-SEAP/Neo vector. Once this vector is transfected into mammalian cells, this vector can then be used as a reporter molecule for GAS binding as described in Examples 13-14.

Other constructs can be made using the above description and replacing GAS with a different promoter sequence. For example, construction of reporter molecules containing NFK-B and EGR promoter sequences are described in Examples 15 and 16. However, many other promoters can be substituted using the protocols described in these Examples. For instance, SRE, IL-2, NFAT, or Osteocalcin promoters can be substituted, alone or in combination (e.g., GAS/NF-KB/EGR, GAS/NF-KB, IL-2/NFAT, or NF-KB/GAS). Similarly, other cell lines can be used to test reporter construct activity, such as HELA (epithelial), HUVEC (endothelial), Reh (B-cell), Saos-2 (osteoblast), HUVAC (aortic), or Cardiomyocyte.

**Example 13: High-Throughput Screening Assay for T-cell Activity.**

The following protocol is used to assess T-cell activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate T-cells. T-cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The T-cell used in this assay is Jurkat T-cells (ATCC Accession No. TIB-152), although Molt-3 cells (ATCC Accession No. CRL-1552) and Molt-4 cells (ATCC Accession No. CRL-1582) cells can also be used.

Jurkat T-cells are lymphoblastic CD4+ Th1 helper cells. In order to generate stable cell lines, approximately 2 million Jurkat cells are transfected with the GAS-SEAP/neo vector using DMRIE-C (Life Technologies)(transfection procedure described below). The transfected cells are seeded to a density of approximately 20,000 cells per well and transfectants resistant to 1 mg/ml genticin selected. Resistant colonies are expanded and then tested for their response to increasing concentrations of interferon gamma. The dose response of a selected clone is demonstrated.

Specifically, the following protocol will yield sufficient cells for 75 wells containing 200 ul of cells. Thus, it is either scaled up, or performed in multiple to generate sufficient cells for multiple 96 well plates. Jurkat cells are maintained in RPMI + 10% serum with 1%Pen-Strep. Combine 2.5 mls of OPTI-MEM (Life Technologies)

with 10 ug of plasmid DNA in a T25 flask. Add 2.5 ml OPTI-MEM containing 50 ul of DMRIE-C and incubate at room temperature for 15-45 mins.

- During the incubation period, count cell concentration, spin down the required number of cells ( $10^7$  per transfection), and resuspend in OPTI-MEM to a final 5 concentration of  $10^7$  cells/ml. Then add 1ml of  $1 \times 10^7$  cells in OPTI-MEM to T25 flask and incubate at 37°C for 6 hrs. After the incubation, add 10 ml of RPMI + 15% serum.

The Jurkat:GAS-SEAP stable reporter lines are maintained in RPMI + 10% serum, 1 mg/ml Genticin, and 1% Pen-Strep. These cells are treated with supernatants containing a polypeptide as produced by the protocol described in Example 11.

- 10 On the day of treatment with the supernatant, the cells should be washed and resuspended in fresh RPMI + 10% serum to a density of 500,000 cells per ml. The exact number of cells required will depend on the number of supernatants being screened. For one 96 well plate, approximately 10 million cells (for 10 plates, 100 million cells) are required.
- 15 Transfer the cells to a triangular reservoir boat, in order to dispense the cells into a 96 well dish, using a 12 channel pipette. Using a 12 channel pipette, transfer 200 ul of cells into each well (therefore adding 100,000 cells per well).
- 20 After all the plates have been seeded, 50 ul of the supernatants are transferred directly from the 96 well plate containing the supernatants into each well using a 12 channel pipette. In addition, a dose of exogenous interferon gamma (0.1, 1.0, 10 ng) is added to wells H9, H10, and H11 to serve as additional positive controls for the assay.
- 25 The 96 well dishes containing Jurkat cells treated with supernatants are placed in an incubator for 48 hrs (note: this time is variable between 48-72 hrs). 35 ul samples from each well are then transferred to an opaque 96 well plate using a 12 channel pipette. The opaque plates should be covered (using sellophene covers) and stored at -20°C until SEAP assays are performed according to Example 17. The plates containing the remaining treated cells are placed at 4°C and serve as a source of material for repeating the assay on a specific well if desired.
- 30 As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate Jurkat T cells. Over 30 fold induction is typically observed in the positive control wells.

**Example 14: High-Throughput Screening Assay Identifying Myeloid Activity**

The following protocol is used to assess myeloid activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate myeloid cells.

- 5 Myeloid cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jak-STATS signal transduction pathway. The myeloid cell used in this assay is U937, a pre-monocyte cell line, although TF-1, HL60, or KG1 can be used.

To transiently transfet U937 cells with the GAS/SEAP/Neo construct produced in Example 12, a DEAE-Dextran method (Kharbanda et. al., 1994, Cell Growth & Differentiation, 5:259-265) is used. First, harvest  $2 \times 10^7$  U937 cells and wash with PBS. The U937 cells are usually grown in RPMI 1640 medium containing 10% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 mg/ml streptomycin.

- 10 Next, suspend the cells in 1 ml of 20 mM Tris-HCl (pH 7.4) buffer containing 0.5 mg/ml DEAE-Dextran, 8 ug GAS-SEAP2 plasmid DNA, 140 mM NaCl, 5 mM KCl, 375 uM  $\text{Na}_2\text{HPO}_4 \cdot 7\text{H}_2\text{O}$ , 1 mM  $\text{MgCl}_2$ , and 675 uM  $\text{CaCl}_2$ . Incubate at 37°C for 45 min.

15 Wash the cells with RPMI 1640 medium containing 10% FBS and then resuspend in 10 ml complete medium and incubate at 37°C for 36 hr.

The GAS-SEAP/U937 stable cells are obtained by growing the cells in 400 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 400 ug/ml G418 for couple of passages.

- 20 These cells are tested by harvesting  $1 \times 10^8$  cells (this is enough for ten 96-well plates assay) and wash with PBS. Suspend the cells in 200 ml above described growth medium, with a final density of  $5 \times 10^5$  cells/ml. Plate 200 ul cells per well in the 96-well plate (or  $1 \times 10^5$  cells/well).

25 Add 50 ul of the supernatant prepared by the protocol described in Example 11. Incubate at 37°C for 48 to 72 hr. As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate U937 cells. Over 30 fold induction is typically observed in the positive control wells. SEAP assay the supernatant according to the protocol described in Example 17.

**Example 15: High-Throughput Screening Assay Identifying Neuronal Activity.**

When cells undergo differentiation and proliferation, a group of genes are activated through many different signal transduction pathways. One of these genes,

- 5 EGR1 (early growth response gene 1), is induced in various tissues and cell types upon activation. The promoter of EGR1 is responsible for such induction. Using the EGR1 promoter linked to reporter molecules, activation of cells can be assessed.

Particularly, the following protocol is used to assess neuronal activity in PC12 cell lines. PC12 cells (rat phenochromocytoma cells) are known to proliferate and/or 10 differentiate by activation with a number of mitogens, such as TPA (tetradecanoyl phorbol acetate), NGF (nerve growth factor), and EGF (epidermal growth factor). The EGR1 gene expression is activated during this treatment. Thus, by stably transfecting PC12 cells with a construct containing an EGR promoter linked to SEAP reporter, activation of PC12 cells can be assessed.

- 15 The EGR/SEAP reporter construct can be assembled by the following protocol. The EGR-1 promoter sequence (-633 to +1)(Sakamoto K et al., Oncogene 6:867-871 (1991)) can be PCR amplified from human genomic DNA using the following primers:
- 5' GCGCTCGAGGGATGACAGCGATAGAACCCGG -3' (SEQ ID NO:6)  
5' GCGAAGCTTCGCGACTCCCCGGATCCGCCTC-3' (SEQ ID NO:7)

20 Using the GAS:SEAP/Neo vector produced in Example 12, EGR1 amplified product can then be inserted into this vector. Linearize the GAS:SEAP/Neo vector using restriction enzymes XhoI/HindIII, removing the GAS/SV40 stuffer. Restrict the EGR1 amplified product with these same enzymes. Ligate the vector and the EGR1 promoter.

- 25 To prepare 96 well-plates for cell culture, two mls of a coating solution (1:30 dilution of collagen type I (Upstate Biotech Inc. Cat#08-115) in 30% ethanol (filter sterilized)) is added per one 10 cm plate or 50 ml per well of the 96-well plate, and allowed to air dry for 2 hr.

PC12 cells are routinely grown in RPMI-1640 medium (Bio Whittaker) 30 containing 10% horse serum (JRH BIOSCIENCES, Cat. # 12449-78P), 5% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 ug/ml streptomycin on a precoated 10 cm tissue culture dish. One to four split is done every three to four days. Cells are removed from the plates by scraping and resuspended with pipetting up and down for more than 15 times.

- 35 Transfect the EGR/SEAP/Neo construct into PC12 using the Lipofectamine protocol described in Example 11. EGR-SEAP/PC12 stable cells are obtained by growing the cells in 300 ug/ml G418. The G418-free medium is used for routine

growth but every one to two months, the cells should be re-grown in 300 ug/ml G418 for couple of passages.

To assay for neuronal activity, a 10 cm plate with cells around 70 to 80% confluent is screened by removing the old medium. Wash the cells once with PBS (Phosphate buffered saline). Then starve the cells in low serum medium (RPMI-1640 containing 1% horse serum and 0.5% FBS with antibiotics) overnight.

The next morning, remove the medium and wash the cells with PBS. Scrape off the cells from the plate, suspend the cells well in 2 ml low serum medium. Count the cell number and add more low serum medium to reach final cell density as  $5 \times 10^5$  cells/ml.

Add 200 ul of the cell suspension to each well of 96-well plate (equivalent to  $1 \times 10^5$  cells/well). Add 50 ul supernatant produced by Example 11, 37°C for 48 to 72 hr. As a positive control, a growth factor known to activate PC12 cells through EGR can be used, such as 50 ng/ul of Neuronal Growth Factor (NGF). Over fifty-fold induction of SEAP is typically seen in the positive control wells. SEAP assay the supernatant according to Example 17.

#### Example 16: High-Throughput Screening Assay for T-cell Activity

NF- $\kappa$ B (Nuclear Factor  $\kappa$ B) is a transcription factor activated by a wide variety of agents including the inflammatory cytokines IL-1 and TNF, CD30 and CD40, lymphotoxin-alpha and lymphotoxin-beta, by exposure to LPS or thrombin, and by expression of certain viral gene products. As a transcription factor, NF- $\kappa$ B regulates the expression of genes involved in immune cell activation, control of apoptosis (NF- $\kappa$ B appears to shield cells from apoptosis), B and T-cell development, anti-viral and antimicrobial responses, and multiple stress responses.

In non-stimulated conditions, NF-  $\kappa$ B is retained in the cytoplasm with I- $\kappa$ B (Inhibitor  $\kappa$ B). However, upon stimulation, I-  $\kappa$ B is phosphorylated and degraded, causing NF-  $\kappa$ B to shuttle to the nucleus, thereby activating transcription of target genes. Target genes activated by NF-  $\kappa$ B include IL-2, IL-6, GM-CSF, ICAM-1 and class 1 MHC.

Due to its central role and ability to respond to a range of stimuli, reporter constructs utilizing the NF- $\kappa$ B promoter element are used to screen the supernatants produced in Example 11. Activators or inhibitors of NF- $\kappa$ B would be useful in treating

diseases. For example, inhibitors of NF- $\kappa$ B could be used to treat those diseases related to the acute or chronic activation of NF- $\kappa$ B, such as rheumatoid arthritis.

- To construct a vector containing the NF- $\kappa$ B promoter element, a PCR based strategy is employed. The upstream primer contains four tandem copies of the NF- $\kappa$ B binding site (GGGGACTTCCC) (SEQ ID NO:8), 18 bp of sequence complementary to the 5' end of the SV40 early promoter sequence, and is flanked with an XhoI site:
- 5':GCGGCCTCGAGGGGACTTCCGGGGACTTCCGGGGACTTCCGGGAC  
TTCCATCCTGCCATCTCAATTAG:3' (SEQ ID NO:9)

- The downstream primer is complementary to the 3' end of the SV40 promoter and is flanked with a Hind III site:

5':GCGGCAAGCTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)

- PCR amplification is performed using the SV40 promoter template present in the pB-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI and Hind III and subcloned into BLSK2-. (Stratagene)
- 15 Sequencing with the T7 and T3 primers confirms the insert contains the following sequence:

5':CTCGAGGGGACTTCCGGGGACTTCCGGGGACTTCCGGGACTTCC  
ATCTGCCATCTCAATTAGTCAGCAACCATACTCCGCCCTAACTCCGCCA  
20 TCCCGCCCTAACTCCGCCAGTCCGCCATTCTCCGCCCATGGCTGACT  
AATTTTTTTATTATGCAGAGGCCAGGCCCTGGCCTTGAGCTATT  
CAGAAGTAGTGAGGAGGCTTTGGAGGCCTAGGCTTGCAAAAAGCTT:  
3' (SEQ ID NO:10)

- 25 Next, replace the SV40 minimal promoter element present in the pSEAP2- promoter plasmid (Clontech) with this NF- $\kappa$ B/SV40 fragment using XhoI and HindIII. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

- In order to generate stable mammalian cell lines, the NF- $\kappa$ B/SV40/SEAP cassette is removed from the above NF- $\kappa$ B/SEAP vector using restriction enzymes SalI and NotI, and inserted into a vector containing neomycin resistance. Particularly, the NF- $\kappa$ B/SV40/SEAP cassette was inserted into pGFP-1 (Clontech), replacing the GFP gene, after restricting pGFP-1 with SalI and NotI.

Once NF- $\kappa$ B/SV40/SEAP/Neo vector is created, stable Jurkat T-cells are created and maintained according to the protocol described in Example 13. Similarly, the method for assaying supernatants with these stable Jurkat T-cells is also described in Example 13. As a positive control, exogenous TNF alpha (0.1, 1, 10 ng) is added to wells H9, H10, and H11, with a 5-10 fold activation typically observed.

**Example 17: Assay for SEAP Activity**

As a reporter molecule for the assays described in Examples 13-16, SEAP activity is assayed using the Tropix Phospho-light Kit (Cat. BP-400) according to the following general procedure. The Tropix Phospho-light Kit supplies the Dilution, Assay, and Reaction Buffers used below.

Prime a dispenser with the 2.5x Dilution Buffer and dispense 15  $\mu$ l of 2.5x dilution buffer into Optiplates containing 35  $\mu$ l of a supernatant. Seal the plates with a plastic sealer and incubate at 65°C for 30 min. Separate the Optiplates to avoid uneven heating.

Cool the samples to room temperature for 15 minutes. Empty the dispenser and prime with the Assay Buffer. Add 50  $\mu$ l Assay Buffer and incubate at room temperature 5 min. Empty the dispenser and prime with the Reaction Buffer (see the table below). Add 50  $\mu$ l Reaction Buffer and incubate at room temperature for 20 minutes. Since the intensity of the chemiluminescent signal is time dependent, and it takes about 10 minutes to read 5 plates on luminometer, one should treat 5 plates at each time and start the second set 10 minutes later.

Read the relative light unit in the luminometer. Set H12 as blank, and print the results. An increase in chemiluminescence indicates reporter activity.

25

**Reaction Buffer Formulation:**

# of plates	Rxn buffer diluent (ml)	CSPD (ml)
10	60	3
11	65	3.25
12	70	3.5
13	75	3.75
14	80	4
15	85	4.25
16	90	4.5
17	95	4.75
18	100	5
19	105	5.25
20	110	5.5
21	115	5.75
22	120	6

23	125	6.25
24	130	6.5
25	135	6.75
26	140	7
27	145	7.25
28	150	7.5
29	155	7.75
30	160	8
31	165	8.25
32	170	8.5
33	175	8.75
34	180	9
35	185	9.25
36	190	9.5
37	195	9.75
38	200	10
39	205	10.25
40	210	10.5
41	215	10.75
42	220	11
43	225	11.25
44	230	11.5
45	235	11.75
46	240	12
47	245	12.25
48	250	12.5
49	255	12.75
50	260	13

**Example 18: High-Throughput Screening Assay Identifying Changes in Small Molecule Concentration and Membrane Permeability**

Binding of a ligand to a receptor is known to alter intracellular levels of small molecules, such as calcium, potassium, sodium, and pH, as well as alter membrane potential. These alterations can be measured in an assay to identify supernatants which bind to receptors of a particular cell. Although the following protocol describes an assay for calcium, this protocol can easily be modified to detect changes in potassium, sodium, pH, membrane potential, or any other small molecule which is detectable by a fluorescent probe.

The following assay uses Fluorometric Imaging Plate Reader ("FLIPR") to measure changes in fluorescent molecules (Molecular Probes) that bind small molecules. Clearly, any fluorescent molecule detecting a small molecule can be used instead of the calcium fluorescent molecule, fluo-3, used here.

For adherent cells, seed the cells at 10,000 -20,000 cells/well in a Co-star black 96-well plate with clear bottom. The plate is incubated in a CO<sub>2</sub> incubator for 20 hours. The adherent cells are washed two times in Biotek washer with 200 ul of HBSS (Hank's Balanced Salt Solution) leaving 100 ul of buffer after the final wash.

A stock solution of 1 mg/ml fluo-3 is made in 10% pluronic acid DMSO. To load the cells with fluo-3, 50 ul of 12 ug/ml fluo-3 is added to each well. The plate is incubated at 37°C in a CO<sub>2</sub> incubator for 60 min. The plate is washed four times in the Bioteck washer with HBSS leaving 100 ul of buffer.

- 5       For non-adherent cells, the cells are spun down from culture media. Cells are re-suspended to 2-5x10<sup>6</sup> cells/ml with HBSS in a 50-ml conical tube. 4 ul of 1 mg/ml fluo-3 solution in 10% pluronic acid DMSO is added to each ml of cell suspension. The tube is then placed in a 37°C water bath for 30-60 min. The cells are washed twice with HBSS, resuspended to 1x10<sup>6</sup> cells/ml, and dispensed into a microplate, 100  
10 ul/well. The plate is centrifuged at 1000 rpm for 5 min. The plate is then washed once in Denley CellWash with 200 ul, followed by an aspiration step to 100 ul final volume.  
For a non-cell based assay, each well contains a fluorescent molecule, such as fluo-3. The supernatant is added to the well, and a change in fluorescence is detected.  
To measure the fluorescence of intracellular calcium, the FLIPR is set for the  
15 following parameters: (1) System gain is 300-800 mW; (2) Exposure time is 0.4 second; (3) Camera F/stop is F/2; (4) Excitation is 488 nm; (5) Emission is 530 nm; and (6) Sample addition is 50 ul. Increased emission at 530 nm indicates an extracellular signaling event which has resulted in an increase in the intracellular Ca<sup>++</sup> concentration.

20      **Example 19: High-Throughput Screening Assay Identifying Tyrosine Kinase Activity**

The Protein Tyrosine Kinases (PTK) represent a diverse group of transmembrane and cytoplasmic kinases. Within the Receptor Protein Tyrosine Kinase (RPTK) group are receptors for a range of mitogenic and metabolic growth factors including the PDGF, FGF, EGF, NGF, HGF and Insulin receptor subfamilies. In addition there are a large family of RPTKs for which the corresponding ligand is unknown. Ligands for RPTKs include mainly secreted small proteins, but also membrane-bound and extracellular matrix proteins.

30      Activation of RPTK by ligands involves ligand-mediated receptor dimerization, resulting in transphosphorylation of the receptor subunits and activation of the cytoplasmic tyrosine kinases. The cytoplasmic tyrosine kinases include receptor associated tyrosine kinases of the src-family (e.g., src, yes, lck, lyn, fyn) and non-receptor linked and cytosolic protein tyrosine kinases, such as the Jak family, members  
35     of which mediate signal transduction triggered by the cytokine superfamily of receptors (e.g., the Interleukins, Interferons, GM-CSF, and Leptin).

Because of the wide range of known factors capable of stimulating tyrosine kinase activity, the identification of novel human secreted proteins capable of activating tyrosine kinase signal transduction pathways are of interest. Therefore, the following protocol is designed to identify those novel human secreted proteins capable of activating the tyrosine kinase signal transduction pathways.

5 Seed target cells (e.g., primary keratinocytes) at a density of approximately 25,000 cells per well in a 96 well Loprodynne Silent Screen Plates purchased from Nalge Nunc (Naperville, IL). The plates are sterilized with two 30 minute rinses with 100% ethanol, rinsed with water and dried overnight. Some plates are coated for 2 hr  
10 with 100 ml of cell culture grade type I collagen (50 mg/ml), gelatin (2%) or polylysine (50 mg/ml), all of which can be purchased from Sigma Chemicals (St. Louis, MO) or 10% Matrigel purchased from Becton Dickinson (Bedford,MA), or calf serum, rinsed with PBS and stored at 4°C. Cell growth on these plates is assayed by seeding 5,000 cells/well in growth medium and indirect quantitation of cell number through use of  
15 alamarBlue as described by the manufacturer Alamar Biosciences, Inc. (Sacramento, CA) after 48 hr. Falcon plate covers #3071 from Becton Dickinson (Bedford,MA) are used to cover the Loprodynne Silent Screen Plates. Falcon Microtest III cell culture plates can also be used in some proliferation experiments.

To prepare extracts, A431 cells are seeded onto the nylon membranes of  
20 Loprodynne plates (20,000/200ml/well) and cultured overnight in complete medium. Cells are quiesced by incubation in serum-free basal medium for 24 hr. After 5-20 minutes treatment with EGF (60ng/ml) or 50 ul of the supernatant produced in Example 11, the medium was removed and 100 ml of extraction buffer ((20 mM HEPES pH 7.5, 0.15 M NaCl, 1% Triton X-100, 0.1% SDS, 2 mM Na<sub>3</sub>VO<sub>4</sub>, 2 mM Na<sub>4</sub>P<sub>2</sub>O<sub>7</sub>)  
25 and a cocktail of protease inhibitors (# 1836170) obtained from Boehringer Mannheim (Indianapolis, IN) is added to each well and the plate is shaken on a rotating shaker for 5 minutes at 4°C. The plate is then placed in a vacuum transfer manifold and the extract filtered through the 0.45 mm membrane bottoms of each well using house vacuum. Extracts are collected in a 96-well catch/assay plate in the bottom of the vacuum  
30 manifold and immediately placed on ice. To obtain extracts clarified by centrifugation, the content of each well, after detergent solubilization for 5 minutes, is removed and centrifuged for 15 minutes at 4°C at 16,000 x g.

Test the filtered extracts for levels of tyrosine kinase activity. Although many methods of detecting tyrosine kinase activity are known, one method is described here.  
35 Generally, the tyrosine kinase activity of a supernatant is evaluated by determining its ability to phosphorylate a tyrosine residue on a specific substrate (a

biotinylated peptide). Biotinylated peptides that can be used for this purpose include PSK1 (corresponding to amino acids 6-20 of the cell division kinase cdc2-p34) and PSK2 (corresponding to amino acids 1-17 of gastrin). Both peptides are substrates for a range of tyrosine kinases and are available from Boehringer Mannheim.

- 5       The tyrosine kinase reaction is set up by adding the following components in order. First, add 10ul of 5uM Biotinylated Peptide, then 10ul ATP/Mg<sub>2+</sub> (5mM ATP/50mM MgCl<sub>2</sub>), then 10ul of 5x Assay Buffer (40mM imidazole hydrochloride, pH7.3, 40 mM beta-glycerophosphate, 1mM EGTA, 100mM MgCl<sub>2</sub>, 5 mM MnCl<sub>2</sub>, 0.5 mg/ml BSA), then 5ul of Sodium Vanadate(1mM), and then 5ul of water. Mix the  
10 components gently and preincubate the reaction mix at 30°C for 2 min. Initiate the reaction by adding 10ul of the control enzyme or the filtered supernatant.

The tyrosine kinase assay reaction is then terminated by adding 10 ul of 120mM EDTA and place the reactions on ice.

- 15      Tyrosine kinase activity is determined by transferring 50 ul aliquot of reaction mixture to a microtiter plate (MTP) module and incubating at 37°C for 20 min. This allows the streptavidin coated 96 well plate to associate with the biotinylated peptide. Wash the MTP module with 300ul/well of PBS four times. Next add 75 ul of anti-phosphotyrosine antibody conjugated to horse radish peroxidase(anti-P-Tyr-POD(0.5u/ml)) to each well and incubate at 37°C for one hour. Wash the well as  
20 above.

- 25      Next add 100ul of peroxidase substrate solution (Boehringer Mannheim) and incubate at room temperature for at least 5 mins (up to 30 min). Measure the absorbance of the sample at 405 nm by using ELISA reader. The level of bound peroxidase activity is quantitated using an ELISA reader and reflects the level of tyrosine kinase activity.

**Example 20: High-Throughput Screening Assay Identifying Phosphorylation Activity**

- As a potential alternative and/or compliment to the assay of protein tyrosine kinase activity described in Example 19, an assay which detects activation (phosphorylation) of major intracellular signal transduction intermediates can also be used. For example, as described below one particular assay can detect tyrosine phosphorylation of the Erk-1 and Erk-2 kinases. However, phosphorylation of other molecules, such as Raf, JNK, p38 MAP, Map kinase kinase (MEK), MEK kinase,  
30     Src, Muscle specific kinase (MuSK), IRAK, Tec, and Janus, as well as any other  
35

phosphoserine, phosphotyrosine, or phosphothreonine molecule, can be detected by substituting these molecules for Erk-1 or Erk-2 in the following assay.

- Specifically, assay plates are made by coating the wells of a 96-well ELISA plate with 0.1ml of protein G (1ug/ml) for 2 hr at room temp, (RT). The plates are then rinsed with PBS and blocked with 3% BSA/PBS for 1 hr at RT. The protein G plates are then treated with 2 commercial monoclonal antibodies (100ng/well) against Erk-1 and Erk-2 (1 hr at RT) (Santa Cruz Biotechnology). (To detect other molecules, this step can easily be modified by substituting a monoclonal antibody detecting any of the above described molecules.) After 3-5 rinses with PBS, the plates are stored at 4°C until use.

- A431 cells are seeded at 20,000/well in a 96-well Loprodyn filterplate and cultured overnight in growth medium. The cells are then starved for 48 hr in basal medium (DMEM) and then treated with EGF (6ng/well) or 50 ul of the supernatants obtained in Example 11 for 5-20 minutes. The cells are then solubilized and extracts filtered directly into the assay plate.

- After incubation with the extract for 1 hr at RT, the wells are again rinsed. As a positive control, a commercial preparation of MAP kinase (10ng/well) is used in place of A431 extract. Plates are then treated with a commercial polyclonal (rabbit) antibody (1ug/ml) which specifically recognizes the phosphorylated epitope of the Erk-1 and Erk-2 kinases (1 hr at RT). This antibody is biotinylated by standard procedures. The bound polyclonal antibody is then quantitated by successive incubations with Europium-streptavidin and Europium fluorescence enhancing reagent in the Wallac DELFIA instrument (time-resolved fluorescence). An increased fluorescent signal over background indicates a phosphorylation.

25

**Example 21: Method of Determining Alterations in a Gene Corresponding to a Polynucleotide**

- RNA isolated from entire families or individual patients presenting with a phenotype of interest (such as a disease) is isolated. cDNA is then generated from these RNA samples using protocols known in the art. (See, Sambrook.) The cDNA is then used as a template for PCR, employing primers surrounding regions of interest in SEQ ID NO:X. Suggested PCR conditions consist of 35 cycles at 95°C for 30 seconds; 60-120 seconds at 52-58°C; and 60-120 seconds at 70°C, using buffer solutions described in Sidransky, D., et al., Science 252:706 (1991).

35

PCR products are then sequenced using primers labeled at their 5' end with T4 polynucleotide kinase, employing SequiTHERM Polymerase. (Epicentre Technologies).

The intron-exon borders of selected exons is also determined and genomic PCR products analyzed to confirm the results. PCR products harboring suspected mutations is then cloned and sequenced to validate the results of the direct sequencing.

- PCR products is cloned into T-tailed vectors as described in Holton, T.A. and 5 Graham, M.W., Nucleic Acids Research, 19:1156 (1991) and sequenced with T7 polymerase (United States Biochemical). Affected individuals are identified by mutations not present in unaffected individuals.
- Genomic rearrangements are also observed as a method of determining alterations in a gene corresponding to a polynucleotide. Genomic clones isolated 10 according to Example 2 are nick-translated with digoxigeninideoxy-uridine 5'-triphosphate (Boehringer Manheim), and FISH performed as described in Johnson, Cg. et al., Methods Cell Biol. 35:73-99 (1991). Hybridization with the labeled probe is carried out using a vast excess of human cot-1 DNA for specific hybridization to the corresponding genomic locus.
- 15 Chromosomes are counterstained with 4,6-diamino-2-phenylidole and propidium iodide, producing a combination of C- and R-bands. Aligned images for precise mapping are obtained using a triple-band filter set (Chroma Technology, Brattleboro, VT) in combination with a cooled charge-coupled device camera (Photometrics, Tucson, AZ) and variable excitation wavelength filters. (Johnson, Cv. 20 et al., Genet. Anal. Tech. Appl., 8:75 (1991).) Image collection, analysis and chromosomal fractional length measurements are performed using the ISee Graphical Program System. (Inovision Corporation, Durham, NC.) Chromosome alterations of the genomic region hybridized by the probe are identified as insertions, deletions, and translocations. These alterations are used as a diagnostic marker for an associated 25 disease.

**Example 22: Method of Detecting Abnormal Levels of a Polypeptide in a Biological Sample**

- A polypeptide of the present invention can be detected in a biological sample, 30 and if an increased or decreased level of the polypeptide is detected, this polypeptide is a marker for a particular phenotype. Methods of detection are numerous, and thus, it is understood that one skilled in the art can modify the following assay to fit their particular needs.

- For example, antibody-sandwich ELISAs are used to detect polypeptides in a 35 sample, preferably a biological sample. Wells of a microtiter plate are coated with specific antibodies, at a final concentration of 0.2 to 10 ug/ml. The antibodies are either monoclonal or polyclonal and are produced by the method described in Example 10.

The wells are blocked so that non-specific binding of the polypeptide to the well is reduced.

The coated wells are then incubated for > 2 hours at RT with a sample containing the polypeptide. Preferably, serial dilutions of the sample should be used to validate results. The plates are then washed three times with deionized or distilled water to remove unbounded polypeptide.

5 Next, 50 ul of specific antibody-alkaline phosphatase conjugate, at a concentration of 25-400 ng, is added and incubated for 2 hours at room temperature. The plates are again washed three times with deionized or distilled water to remove 10 unbounded conjugate.

15 Add 75 ul of 4-methylumbelliferyl phosphate (MUP) or p-nitrophenyl phosphate (NPP) substrate solution to each well and incubate 1 hour at room temperature. Measure the reaction by a microtiter plate reader. Prepare a standard curve, using serial dilutions of a control sample, and plot polypeptide concentration on the X-axis (log scale) and fluorescence or absorbance of the Y-axis (linear scale). Interpolate the concentration of the polypeptide in the sample using the standard curve.

#### **Example 23: Formulating a Polypeptide**

20 The secreted polypeptide composition will be formulated and dosed in a fashion consistent with good medical practice, taking into account the clinical condition of the individual patient (especially the side effects of treatment with the secreted polypeptide alone), the site of delivery, the method of administration, the scheduling of administration, and other factors known to practitioners. The "effective amount" for purposes herein is thus determined by such considerations.

25 As a general proposition, the total pharmaceutically effective amount of secreted polypeptide administered parenterally per dose will be in the range of about 1 µg/kg/day to 10 mg/kg/day of patient body weight, although, as noted above, this will be subject to therapeutic discretion. More preferably, this dose is at least 0.01 mg/kg/day, and most preferably for humans between about 0.01 and 1 mg/kg/day for the hormone. If 30 given continuously, the secreted polypeptide is typically administered at a dose rate of about 1 µg/kg/hour to about 50 µg/kg/hour, either by 1-4 injections per day or by continuous subcutaneous infusions, for example, using a mini-pump. An intravenous bag solution may also be employed. The length of treatment needed to observe changes and the interval following treatment for responses to occur appears to vary depending 35 on the desired effect.

Pharmaceutical compositions containing the secreted protein of the invention are administered orally, rectally, parenterally, intracistemally, intravaginally,

intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), buccally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any type. The term "parenteral" as used herein refers to modes 5 of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

- The secreted polypeptide is also suitably administered by sustained-release systems. Suitable examples of sustained-release compositions include semi-permeable polymer matrices in the form of shaped articles, e.g., films, or mirocapsules.
- 10 Sustained-release matrices include poly lactides (U.S. Pat. No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma-ethyl-L-glutamate (Sidman, U. et al., Biopolymers 22:547-556 (1983)), poly (2-hydroxyethyl methacrylate) (R. Langer et al., J. Biomed. Mater. Res. 15:167-277 (1981), and R. Langer, Chem. Tech. 12:98-105 (1982)), ethylene vinyl acetate (R. Langer et al.) or poly-D-(-)-3-hydroxybutyric 15 acid (EP 133,988). Sustained-release compositions also include liposomally entrapped polypeptides. Liposomes containing the secreted polypeptide are prepared by methods known per se: DE 3,218,121; Epstein et al., Proc. Natl. Acad. Sci. USA 82:3688-3692 (1985); Hwang et al., Proc. Natl. Acad. Sci. USA 77:4030-4034 (1980); EP 52,322; EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese Pat. Appl. 83-118008;
- 20 U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily, the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. percent cholesterol, the selected proportion being adjusted for the optimal secreted polypeptide therapy.

For parenteral administration, in one embodiment, the secreted polypeptide is 25 formulated generally by mixing it at the desired degree of purity, in a unit dosage injectable form (solution, suspension, or emulsion), with a pharmaceutically acceptable carrier, i.e., one that is non-toxic to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation. For example, the formulation preferably does not include oxidizing agents and other compounds that are 30 known to be deleterious to polypeptides.

Generally, the formulations are prepared by contacting the polypeptide uniformly and intimately with liquid carriers or finely divided solid carriers or both. Then, if necessary, the product is shaped into the desired formulation. Preferably the carrier is a parenteral carrier, more preferably a solution that is isotonic with the blood 35 of the recipient. Examples of such carrier vehicles include water, saline, Ringer's solution, and dextrose solution. Non-aqueous vehicles such as fixed oils and ethyl oleate are also useful herein, as well as liposomes.

- The carrier suitably contains minor amounts of additives such as substances that enhance isotonicity and chemical stability. Such materials are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, succinate, acetic acid, and other organic acids or their salts; antioxidants such as ascorbic acid; low molecular weight (less than about ten residues) polypeptides, e.g., polyarginine or tripeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids, such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, glucose, manose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; counterions such as sodium; and/or nonionic surfactants such as polysorbates, poloxamers, or PEG.

10 The secreted polypeptide is typically formulated in such vehicles at a concentration of about 0.1 mg/ml to 100 mg/ml, preferably 1-10 mg/ml, at a pH of about 3 to 8. It will be understood that the use of certain of the foregoing excipients, carriers, or stabilizers will result in the formation of polypeptide salts.

15 Any polypeptide to be used for therapeutic administration can be sterile. Sterility is readily accomplished by filtration through sterile filtration membranes (e.g., 0.2 micron membranes). Therapeutic polypeptide compositions generally are placed 20 into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

25 Polypeptides ordinarily will be stored in unit or multi-dose containers, for example, sealed ampoules or vials, as an aqueous solution or as a lyophilized formulation for reconstitution. As an example of a lyophilized formulation, 10-ml vials are filled with 5 ml of sterile-filtered 1% (w/v) aqueous polypeptide solution, and the resulting mixture is lyophilized. The infusion solution is prepared by reconstituting the lyophilized polypeptide using bacteriostatic Water-for-Injection.

30 The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the polypeptides of the present invention may be employed in conjunction with other therapeutic compounds.

**Example 24: Method of Treating Decreased Levels of the Polypeptide**

It will be appreciated that conditions caused by a decrease in the standard or normal expression level of a secreted protein in an individual can be treated by administering the polypeptide of the present invention, preferably in the secreted form.

- 5 Thus, the invention also provides a method of treatment of an individual in need of an increased level of the polypeptide comprising administering to such an individual a pharmaceutical composition comprising an amount of the polypeptide to increase the activity level of the polypeptide in such an individual.

For example, a patient with decreased levels of a polypeptide receives a daily dose 0.1-100 ug/kg of the polypeptide for six consecutive days. Preferably, the polypeptide is in the secreted form. The exact details of the dosing scheme, based on administration and formulation, are provided in Example 23.

**Example 25: Method of Treating Increased Levels of the Polypeptide**

15 Antisense technology is used to inhibit production of a polypeptide of the present invention. This technology is one example of a method of decreasing levels of a polypeptide, preferably a secreted form, due to a variety of etiologies, such as cancer.

For example, a patient diagnosed with abnormally increased levels of a polypeptide is administered intravenously antisense polynucleotides at 0.5, 1.0, 1.5, 20 2.0 and 3.0 mg/kg day for 21 days. This treatment is repeated after a 7-day rest period if the treatment was well tolerated. The formulation of the antisense polynucleotide is provided in Example 23.

**Example 26: Method of Treatment Using Gene Therapy**

25 One method of gene therapy transplants fibroblasts, which are capable of expressing a polypeptide, onto a patient. Generally, fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in tissue-culture medium and separated into small pieces. Small chunks of the tissue are placed on a wet surface of a tissue culture flask, approximately ten pieces are placed in each flask. The flask is 30 turned upside down, closed tight and left at room temperature over night. After 24 hours at room temperature, the flask is inverted and the chunks of tissue remain fixed to the bottom of the flask and fresh media (e.g., Ham's F12 media, with 10% FBS, penicillin and streptomycin) is added. The flasks are then incubated at 37°C for approximately one week.

At this time, fresh media is added and subsequently changed every several days. After an additional two weeks in culture, a monolayer of fibroblasts emerge. The monolayer is trypsinized and scaled into larger flasks.

5 pMV-7 (Kirschmeier, P.T. et al., DNA, 7:219-25 (1988)), flanked by the long terminal repeats of the Moloney murine sarcoma virus, is digested with EcoRI and HindIII and subsequently treated with calf intestinal phosphatase. The linear vector is fractionated on agarose gel and purified, using glass beads.

10 The cDNA encoding a polypeptide of the present invention can be amplified using PCR primers which correspond to the 5' and 3' end sequences respectively as set forth in Example 1. Preferably, the 5' primer contains an EcoRI site and the 3' primer includes a HindIII site. Equal quantities of the Moloney murine sarcoma virus linear backbone and the amplified EcoRI and HindIII fragment are added together, in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The ligation mixture is then used to 15 transform bacteria HB101, which are then plated onto agar containing kanamycin for the purpose of confirming that the vector has the gene of interest properly inserted.

20 The amphotropic pA317 or GP+am12 packaging cells are grown in tissue culture to confluent density in Dulbecco's Modified Eagles Medium (DMEM) with 10% calf serum (CS), penicillin and streptomycin. The MSV vector containing the gene is then added to the media and the packaging cells transduced with the vector. The 25 packaging cells now produce infectious viral particles containing the gene (the packaging cells are now referred to as producer cells).

25 Fresh media is added to the transduced producer cells, and subsequently, the media is harvested from a 10 cm plate of confluent producer cells. The spent media, containing the infectious viral particles, is filtered through a millipore filter to remove detached producer cells and this media is then used to infect fibroblast cells. Media is removed from a sub-confluent plate of fibroblasts and quickly replaced with the media from the producer cells. This media is removed and replaced with fresh media. If the titer of virus is high, then virtually all fibroblasts will be infected and no selection is 30 required. If the titer is very low, then it is necessary to use a retroviral vector that has a selectable marker, such as neo or his. Once the fibroblasts have been efficiently infected, the fibroblasts are analyzed to determine whether protein is produced.

35 The engineered fibroblasts are then transplanted onto the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads.

It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples. Numerous modifications and

variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the appended claims.

- The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, or other disclosures) in the Background of the Invention, Detailed Description, and Examples is hereby incorporated herein by reference.
- 5

(1) GENERAL INFORMATION:

110

	GGGATCCGGA GCCCCAAATCT TCTGACAAAAA CTCACACATG CCCACCGTGC CCAGCACCTG	60
	AATTGAGGG TGCACCGTCA GTCTTCCTCT TCCCCCAAA ACCAAGGAC ACCCTCATGA	120
5	TCTCCCGGAC TCCTGAGGTTC ACATGCGTGG TGGTGGACGT AAGCCACGAA GACCCGTGAGG	180
	TCAAGTTCAA CTGGTACGTG GACGGCGTGG AGGTGCTAA TGCCAAGACA AAGCCGGGG	240
10	AGGAGCAGTA CAACAGCACG TACCGTGTGG TCAGCGTCCT CACCGTCCTG CACCAGGACT	300
	GGCTGAATGG CAAGGAGTAC AAGTGCAAGG TCTCCAACAA AGCCCTCCC ACCCCCACG	360
	AGAAAACCAT CTCCAAAGCC AAAGGGCAGC CCCGAGAAC ACAGGTGTAC ACCCTGCC	420
15	CATCCCGGGA TGAGCTGACC AAGAACCAAGG TCAGCCTGAC CTGCTGGTC AAAGGCTTCT	480
	ATCCAAGCGA CATGCCGTG GAGTGGGAGA GCAATGGCA GCCGGAGAAC AACTACAAGA	540
20	CCACGCCCTCC CGTGCTGGAC TCCGACGGCT CCTTCTTCCT CTACAGCAAG CTCACCGTGG	600
	ACAAGAGCAG GTGGCAGCAG GGGAACGTCT TCTCATGCTC CGTGATGCAT GAGGCTCTGC	660
	ACAACCACTA CACCGAGAAG AGCCTCTCCC TGTCTCCGGG TAAATGAGTG CGACGGCCGC	720
25	GACTCTAGAG GAT	733

30 (2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 5 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Trp Ser Xaa Trp Ser  
 1                   5

40 (2) INFORMATION FOR SEQ ID NO: 3:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 86 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GGGCCTCGAG ATTTCCCCGA AATCTAGATT TCCCCGAAAT GATTCCCCG AAATGATTTC	60
55 CCCGAAATAT CTGCCATCTC AATTAG	86

60 (2) INFORMATION FOR SEQ ID NO: 4:

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

10 GCGGCAAGCT TTTTCAAAG CCTAGGC 27

15 (2) INFORMATION FOR SEQ ID NO: 5:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 271 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

25 CTCGAGATTT CCCGAAATC TAGATTTCCC CGAAATGATT TCCCCGAAAT GATTTCCCG 60  
AAATATCTGC CATCTCAATT AGTCAGCAAC CATACTCCCG CCCCTAACTC CGCCCATCC 120  
GCCCTTAACT CCGCCCAGTT CCGCCCATTC TCCGCCCCAT GGCTGACTAA TTTTTTTTAT 180  
30 TTATGCAGAG GCCGAGGCCG CCTCGGCCTC TGAGCTATTC CAGAAGTAGT GAGGAGGCTT 240  
TTTGAGGC CTAGGCTTTT GCAAAAGCT T 271

35 (2) INFORMATION FOR SEQ ID NO: 6:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

45 GCGCTCGAGG GATGACAGCG ATAGAACCCC GG 32

50 (2) INFORMATION FOR SEQ ID NO: 7:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GCGAAGCTTC GCGACTCCCC GGATCCGCCT C

31

## 5 (2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 12 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

15 GGGGACTTTC CC 12

## 20 (2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 73 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

30 GCGGCCTCGA GGGGACTTTC CGGGGGACTT TCCGGGGACT TTCCGGGACT TTCCATCCTG 60  
CCATCTCAAT TAG 73

## 35 (2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 256 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

45 CTCGAGGGGA CTTCCTCCGG GACTTTCCGG GGACTTTCCG GGACTTTCCA TCTGCCATCT 60  
CAATTAGTCA GCAACCATAG TCCCGCCCT AACTCCGCC ATCCCGCCC TAACTCCGCC 120  
50 CAGTTCCGCC CATTCTCCGC CCCATGGCTG ACTAATTTTT TTTATTTATG CAGAGGCCGA 180  
GGCCGCCTCG GCCTCTGAGC TATTCCAGAA GTAGTGAGGA GGCTTTTTG GAGGCCTAGG 240  
CTTTTGCAAA AAGCTT 256

## 55

## (2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2084 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

	CTATCAGATG CTGGGCCTCC TCAGCCATAG CCCCCCTGCTC CTACCCCCCTG ACTGGCTCTT	60
10	GTGTCCCTCAC CTCTCACCCCT CTCCCTTCCTG GGAGGCCCTG GGAGGTGATC ATTGACACCC	120
	AGCCAAGCAG ACAGCTGCGG GTGCCCAAGC CCTTGCTGGG CCTGCGCGTG AGGAGTCCCA	180
	CTGCTTCTAA AGGAAGTCCT GGGCAGGAGG TGGCTTTGGT GGTTGGTCC AAAGTTGAAA	240
15	ATGCTTGCAG TTTGACCTTA GAAGAAGTGG GAAGAAGAAG GAGCTCTACA GGGTCAGCTT	300
	TGTTTGATTT GTCCAGTCTA AGAAGTCCCA TTGCCAAAGC TTTCTGCAGG AGGGTGAATG	360
20	CCGCAGCTTG GCAGCCCTG GGTTCTCTT GGAAATGGTC AGTTTCCCT CAAAGTACCC	420
	AAAGTAGCCT TGGCTTGAGT TTTTGTCCCT GCCTCCTTT TAGAGAAGAG GGCATTTAGA	480
	CTGCATTTTC CTGGTTAAAG AAGGTTAAAG CAAATGTTA TTGCCCTTTTC TAGTGAACTA	540
25	ACTCGTAGAG ATGTTCTCAG CAGGAAGACA GTCTTAGCAC TGTCACTTAG CAGATTGCAC	600
	TTAACGTCCCT TGTGCTGGCC AGATGGCGTG GCTGGTTGCC TTAATATGTC CCAGGACCCC	660
30	TGACAGGGCT GCCTGGCCTC TCCCTCGTGC TCCCTCAAGAG CCCAGTCCAT ACACTGTGGA	720
	TGTCATTGCT GTCGGGTTAG GAAGTCTTGT CCTAGAACGC CCTGGCTGGT ATGACCACAG	780
	TTCATGGCGG CTCTTCTCGC TTGGGTCAAT GTCATCTTCC AGCACCTGCT GTGCTGGGNA	840
35	AGGCCGAGGA TGGGGGCCCA GCACTGTCCA GGCCTGCTGG GGCCTGGCTG GGAGTCCTGT	900
	GGGCAGCATG GAACATGCAG CTGGGCTTCC TGAGGACAGG CACCCCTCTGG CACIGTTGCT	960
40	TGCCCTGTGC CCTGGACCTT TTCCCTGCCCT TCTCCTTCCT CTGCTCCCTT GGGGCTACCC	1020
	CTTGGCCCTT CCTGGTCTGT GCAAACCTCCC TCAGGGAGCC CCCCTGCCCT GTAGCTCTCR	1080
	CTTAACCTTCC TAGGGGCTGC TGAGCCCACC CAGAGTTGT TGGAGTTCAAG CGGGGCAGCT	1140
45	TGTCTCCCTT GTCAGCAGGG GCGTAAGGGC TGGGTTGGC CATACAAGGT TGGCTACGCC	1200
	CTCAATCCCT GACCGTTCCA GGCACGTGAGC TGGGCACCCA CGGAAGGACA TGCTGTCCAG	1260
50	ACTGTGATGA CTGCCAGCAC AGGGCATCTC GGGCTTGGCT GGTCTGCGAG GCCCTGCCCT	1320
	TGTGGAACTC TGGGTTCCCTG TTTTCTCAGT CTTTTTGCG GCTTTGCTGT GGTTGGCAGC	1380
	TGCCGTACTC CAGGCTTGTG TCGGCCACTC AGATGAGGGC TGTGGTGCAG GCCAGTGCAG	1440
55	GAGAGCTGCG CTTGGGATTC TGCCCTCTCC TGTGCTGTC CTCCGGACCT ACCCAGGTCT	1500
	CCACCCATCAG GACCCGTCT TTGGGTTAG AAGACCAAGT ATGGGGAAAA CCAGGCACCA	1560
60	GCCTCTGCAG CAATGGGTCC CTCTAGCCTG TGGACACCAG CTGGGGGATC CAGGGTCAGG	1620

	CCCCCTCCTC TCCCCAGTTT CCCTCTGCTG TGGGTTCTGG GCTGTCATGT CTCCACCACT	1680
	TAAGGATGTC TTTACACTGA CTTCAGGATA GATGCTGGGA TGCCCTGGCA TG GCCACATG	1740
5	TTACATGTAC AGAACTTTGT CTACAGCACA AATTAAGTTA TATAAACACA GTGACTGGTA	1800
	TTTAATGCTG ATCTACTATA AGGTATTCTA TATTTATATG ACTTCAGAGA CGCGTATGTA	1860
10	ATAAAGGACG CCCTCCCTCC AGTGTCCACA TCCAGTTCAC CCCAGAGGGT CGGGCAGGTT	1920
	GACATATTTA TTTTGTCATA TTCTGTAGGC TTCCATGTCC AGAATCCTGC TTAAGGTTTT	1980
	AGGGTACCTT CAGTACTTTT TGCAATAAAA GTATTTCTTA TCCAAAAAAA AAAAAAAA	2040
15	ACTCGAGGGG GGGCCCGGTA CCCAATTGCG CCCTATAAAG AGTC	2084

(2) INFORMATION FOR SEQ ID NO: 12:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

30	AATT CGGCAC CAGGAGAAAGT GGAGTTTGGG AGTT CAGGGG CACAGGGGCA CAGGCCACG	60
	ACTGCAGCGG GATGGACCAG TACTGCATCC TGGGCCCAT CGGGGAGGGC GCCCAMGGCA	120
	TCGTCTCAA GGCCAAGCAC GTGGAGACTG GCGAGATAGT TGCCCTCAAG AAGGTGGCCC	180
35	TAAGGC GGTT GGAAGACGGC TTCCCTAACCC AGGCCCTGCG GGAGATTAAG GCTCTGCAGG	240
	ARATGGAGGA CAATCACTAT GTGGTACAAC TGAAGGCTGT GTTCCCACAC GGTGGAGGCT	300
40	TTGTGCTGGC CTTTGAGTTC ATGCTGTCCG ATCTGCCGA GGTGGTGCAG CATGCCAGA	360
	GGCCACTAGC CCAGGCACAG GTCAAGAGCT ACCTGCAGAT GCTGCTCAAG GGTGTGGCCT	420
	TCTGCCATGC CAACAACATT GTACATCGGG ACCTGAAACC TGCCAAACCTG CTCATCAGCG	480
45	CCTCAGGCCA GCTCAAGATA GCGGACTTTG GCCTGGCTCG AGTCTTTCC CCAGACGGCA	540
	GCCGCCTCTA CACACACCAG GTGGCCACCA GGAGCTCACT GAGCTGCCGG ACTACAACAA	600
	GATCTCCCTT AAGGAGCAGG TGCCCATGCC CCTGGAGGAK GTGCTGCCTG ACGTCTCTCC	660
50	CCAGGCATTG GATCTGCTGG GTCAATTCTT TCTCTACCTT CCTCACCCAGC GCATCGCAGC	720
	TTCCAAGGCT CTCCTCCATC AGTACTTCTT CACAGCTCCC CTGCTGCCCG ATCCATCTGA	780
55	GCTGCCGATT CCTCAGCGTC TAGGGGGACC TGCCCCAAG GCCCATCCAG GGCCCCCCC	840
	CATCCATGAC TTCCACGTGG ACCGGCCCTCT TGAGGARTCG CTGTTGAACC CARARCTGAT	900
60	TCGGCCCTTC ATCCTGGARG GGTGAGAAGT TGGCCCTGGT CCCGTCTGCC TGCTCCTCAG	960

	GACCACTCAG TCCACCTGTT CCTCTGCCAC CTGCCTGGCT TCACCCCTCCA AGGCCTCCCC	1020
	ATGGCCACAG TGGGCCACA CCACACCCAG CCCCTTAGCC CTTGCGAAGG TTGGTCTCGA	1080
5	RGCAGARGTC ATGTTCCCAG CCAAGAGTAT GAGAACATCC AGTCGAGCAG AGGAGATTCA	1140
	TGGCCTGTSC TCGGTGAGCC TTACCTTCIG TGTGCTTCAC ATCACTGAGC ACTCATTTAG	1200
10	AAGTGAGGGA GACAGAAGTC TAGS0CCAGG GATGGCTCCA GTTGGGGATC CAGCAGGAGA	1260
	CCCTCTGCAC ATGAGGCTGG TTTMCCAACA TCTACTCCCT CAGGATGAGC GTGAGCCAGA	1320
	AGCAGCTGTG TATTTAAAGGA AACAAAGCGTT CCTGGAATTA ATTTATAAAAT TTAATAAAATC	1380
15	CCAATATAAT CCCAGCTAGT GCTTTTTCT TATTATAATT TGATAAGGTG ATTATAAAAAG	1440
	ATACATGGAA GGAAGTGGAA CCAGATGCAG AAGAGGAAT GATGGAAGGA CTTATGGTAT	1500
	CAGATACCAA TATTTAAAAG TTGTATAAT AATAAAGAGT ATGATTGTGG TTCAAGGATA	1560
20	AAAAAAAAA AAAAAAAAAA ACTCGA	1586

25 (2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2350 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

35	GAAGAAGAGC GACCTGCCCT AATGGATGAC AGAAAGCACA AAATTTGTAG CATGTATGAC	60
	AACCTTAAGGG GGAAATTGCC TGGACAAGAG AGGCCTAGTG ATGACCACTT TGTACAGATC	120
40	ATGTGTATCC GAAAAGGGAA GAGAATGGTT GCCCGTATTC TTCCCTTCCT CTCCACAGAG	180
	CAAGCAGCTG ACATTCTCAT GACAACAGCC AGGAACCTCC CTTTCCTTAT CAAGAAGGAT	240
	GCACAAGATG AGGTGCTGCC ATGCTTACTG AGTCCCTCT CTCTCCTTCT CTATCATCTT	300
45	CCATCAGTGA GTCATCACCAG CCTTTTGCGA CATAATGAAC CTACCTCAA GTGCAGCTAC	360
	ACCAGCACTC TCCAATCCTC ACCTCACTGC TGTGCTCCAG AACAAAGTTG GCCTGTCACT	420
	GSTCCTCATC CTCCTGAGCC GTGGTGAAGA CCTACAGAGT TCAGACCTG CTACAGAATC	480
50	AACACAAAAT AATCAGTGGA CGGAGGTGAT GTTCATGGCA ACACGAGAAC TTCTGCGGAT	540
	TCCCCAAGCA GCCCTGGCCA AGCCAATCTC TATACCTACA AACCTAGTGT CCCTCTTTTC	600
55	TCGCTATGTT GACCGGCAGA AACTGAACCTT GCTGGAGASA AAACATGCAGC TAGTTCAAGGG	660
	GATACGATAA AAGATCTCCA AATGTGTCT GTACCTCTT TTGGCTGCCA CCTGCACTGC	720
60	TGCCATCACC AATGGRGTGT TTTTAATGAG GGAAGGAAGG TAGCTTTTC CCCAAAGCAA	780

	AGKMTTGTGG GATCGATTCC TGTTTACAGG GGTTGTCTCT CTAATGTCA GATATTTCCC	840
	CACTGCCTCA TGAATTTCGG CTGGGTGATA CCTCTCTGG TTCTTTTACC TTCTGTGTTA	900
5	CAGTTCTGCA TGTCTACTT TTACTCAGTT CTGTTTGCA TTTWCTTTGC CCTAGAGACA	960
	CAAGTGTAAAT CTCTCCCTT ATCCCTCAC TACTCCACCT CAGAGTAGAT TGTAGCCTGC	1020
10	CAAAGGATTC CTTCCCTCAT CCTATTGAAG TTGTTTTTC ATTGCCCAT ATTAATATGA	1080
	CTATAGAAGA GCCAATTAAG TAGAAATCAA GATATACACA CACACATAGA TACACACACA	1140
	CACACCCAT ACATGTATTT ATGTGGTCTT CAGAGGGTCC TTAAAGAATG AATTTTAGAT	1200
15	TGAAAAATAT TTAGTTGTCT CATTACCTCT TCTAAACACA AACCAGCTGA TGTATTTAA	1260
	TCTGTTCTG TTCTATCTG TAATTAATTT GGTTGGTCT ACTTGTTTA ACATAAATAA	1320
20	AGAGTATGCA GCACGTTAA TAAAATCAGA ACTCTTAATT GGCTTATGCC CAGGTCTAGG	1380
	CTGAGAACGTC CTTTTCTTC TTCCCACCTT TATTCCTTA GTTCTGTCC ACCTPAATCG	1440
	AAACAAACACA TGGTTATGTC TTTTCTG TACAACATACA GGGTACTTGA GCCTTCCCC	1500
25	TCAAGTGCAT TCGAAGTCAC CCAGGATGAT CCTCACTAGT AGCCTGCTTT GGCAAGTGTGG	1560
	CTTTTGCAC ACTTGCCCTG TCTTCCTGAG ACTACTTCAG TAAGCCATGC TTCCTCTTC	1620
30	CCCACTTTA TTGGGTGTCA TGAATAGAAA CTTCCAATG TAACCATGGA AGCTAAGTTT	1680
	GGCCTGCTTT GCTTTTAGT CTCCACACCA TGGCAGAAC TGCTGTCTT ACTACTTCAT	1740
	CTCACCCAAG TCCCGTTCCC AGGCAGCCAR GGGCTGGGT TTGAATAAT TGCAAGGGCC	1800
35	AGCCTGCCAT GATCTTCTC ACTTACTCCT CTCCCATTCA GCAATCAACC AGACTAAGGA	1860
	GTTTGTGATCC CTAGTGAATA CAGCCCTGAA GAAAATAAA TCTGAATTAA TTTTACATGG	1920
40	CCTTCGTGAT CTTCTGCTG TTCTTACTTT TTGAAATGTA GTTGGGGGT GGGAGGGACA	1980
	GGTTATGGTA TTTAAAGAGA ATAAACATTG TGACACATACA TGTATIGTAC AACAGTAAGA	2040
	TCCTCTGTTA AAACCAGCTG TCCTGTTCTC CATCTCCATT TCTTCCCATG CTGTAACCCC	2100
45	AGGCTCCACC AGCTGTTCCC CAGTGATGTT ACCTAGCTTC CCTCTACCGT TGTCTACTGA	2160
	CCATTTCCAC TACATGCCTT TCCTACCTTC CCTTCACAAC CAATCAAGTG AATACTTGAT	2220
	TATTATCTCT TCCTTACTGT GCTTATCTT TTTTGTGTTGG ATTGGTTCTA ATTAATGAAA	2280
50	ATAAAAGTTT CTAAATTTAC ATTTTATAG GGTATTGTAA ATAAAAACAA ATTGTATACT	2340
	TAAAAAAAAA	2350
55		

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:  
 60 (A) LENGTH: 1348 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

	ACGAAGACAC CAGACCCGT GGAGCTGTG GTGACCACCG AAGGNCAGTT CGGGTGCAGC	60
10	AGGGCTCGAG CCCAGAAAAC TATCCTCTAA GACCAGACGT GACAAGGAGA AGCAGAGCTG	120
	TAAGAGCTGT GGTGAGACCT TCAACTCCAT CACCAAGAGG AGGCATCACT GCAAGCTGTG	180
	TGGGGCGGTC ATCTGTGGGA AGTGCTCCGA GTTCAAGGCC GAGAACAGCC GGCAGAGCCT	240
15	GTCTGCAGAG ATTGTTTCCT GACACAGCCA GTGGCCCCGT AGAGCACAGA GAAGACACCC	300
	ACTGCAGACC CCCAGCCCCAG CCTGCTCTGC GGCCCCCTGC GGCTGTYAGA GAGCGGTGAG	360
20	ACCTGGAGCG AGGTGTGGC CGCCATCCCC ATGTCAGATC CCCAGGTGCT GCACCTGCAG	420
	GKAGGCAGCC AGGACGGCCG GCTGCCCGC ACCATCCCTC TCCCCAGCTG CAAACTGAGT	480
	GTGCCGGACC CTGAGGAGAG GCTGGACTCG GGGCATGTGT GGAAGCTGCA GTGGGCCAAG	540
25	CAGTCCTGGT ACCTGAGCCG CTCCCTCCGA GAGCTGCAGC AGCAGTGGCT GGAAACCCCTA	600
	AGCACTGCTG CCCATGGGA CACGGCCAG GACAGCCCCG GGGCCCTGCA GCTTCAGGTC	660
30	CCTATGGCG CAGTGCTCCG TGAGCTGAGT CTCCCACCTGC CCTGCACACC ACCACATTGG	720
	ACCTGTGCTG TCCTGGGAGG TGGTGTGGGA GGCCCCATGA AGACGCCCT GGACTTGCTT	780
	GAGGGTGGGC CAACAGCCA GAGYTCAGGA CATTTGGCTT TGGGGGAAG GAAAYTGAGG	840
35	CCCAGAGAGG GGCAACCAYT GGCCAAGGGT CACCCAGCAA GTTTGGYTA AGAGCCTGGC	900
	CTCCAGCCCC AGCAGTKTGG CCCAGAGCAG GGGCCGAYTG CCAAAGTAAC CATCATCCAT	960
40	ATGGGCCGTG TGGTGATGCT GGCCCCGAAG GCAGAAAGAG GCACCATGGG CACTGCCAGG	1020
	GACAGCCACA TCCCTGCTGGT CTGCAGCGTG GTCCACCCCG CCTCTGCCCA GCCTGTCTAC	1080
	ACCGTGTGAG CTGAATCGTG ACTTGCTTCC CACCTCCTTT CTCTGTCTC TCCTGAGGTT	1140
45	CTGCCTGCAG CCCCCAGGAG GTGGCCGTG CCCATCCTAG CTGAGTCAT GTTCCCTAAA	1200
	TAACCACGCT CAGAAGCTCT GCTAGGACTT ACCCCAGCCA CTGAGTGGCA GGCGCATGAG	1260
50	ATTTGTGGCT GTTCCCTGATG CTAGTGGCAC ACAGTGCTTA TCTGCATAAA TAAACACTGG	1320
	SCACCAAAAA AAAAAGAAAA AAAAAGAC	1348

55 (2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1123 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

60

## (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

5	CGCGCCCAGC CCCTGCTGCT CTGGGCAGAC GATGCTGAAG ATGCTCTCCT TTAAGCTGCT	60
	GCTGCTGGCC GTGGCTCTGG GCTTCTTGA AGGAGATGCT AAGTTGGGG AAAGAAACGA	120
10	AGGGAGCGGA GCAAGGAGGA GAAGGTGCCT GAATGGGAAC CCCCCGAAGC GCCTGAAAAG	180
	GAGAGACAGG AGGATGATGT CCCAGCTGGA GCTGCTGACT GGGGGAGAGA TGCTGTGCCG	240
	TGGCTTCTAC CCTCGGCTGT CCTGCTGCCT GCGGAGTGAC AGCCCGGGC TAGGGCGCCT	300
15	GGAGAATAAG ATATTTCTG TTACCAACAA CACAGAATGT GGGAACTTAC TGGAGGAAAT	360
	CAAATGTCCA CTTTGTCTC CACATTCTCA AAGCCTGTC CACTCACCTG AGAGAGAAGT	420
20	CTTGGAAAGA GACCTAGTAC TTCCTCTGCT CTGCAAAGAC TATTGCAAAG AATTCTTTA	480
	CACTTGCCGA GGCCATATTC CAGGTTCCCT TCAAACAACT GCGGATGAGT TTTGCTTTA	540
	CTATGCAAGA AAAGATGGTG GGTTGTGCTT TCCAGATTTT CCAAGAAAAC AAGTCAGAGG	600
25	ACCAGCATCT AACTACTTGG ACCAGATGGA AGAATATGAC AAAGTGGAAAG AGATCAGCAG	660
	AAAGCACAAA CACAACGTCT TCTGTATTCA GGAGGTTGTG AGTGGCTGC GGCAAGCCGT	720
30	TGGTGCCCTG CATACTGGGG ATGGCTCGCA ACGTCTCTC ATTCTGGAAA AAGAAGGTTA	780
	TGTGAAGATA CTTACCCCTG AAGGAGAAAT TTTCAAGGAG CCTTATTGG ACATTACAAA	840
	ACTTGTCAA AGTGGAAATAA AGGTTGGCTT TTTAAATTTT ATTATTTT GTGCTGGCTA	900
35	CGTTAATTTT ATTTTAGTGT TACCTTCCTC ACTGAAGGT TTTCTTTGTA ATAAAAGAAA	960
	GAATCTTGCA GGAGAAAATA AGGGGGCAAC ATAAGAAAACA ATAATTATGG CACCTGAATT	1020
40	AGGACAGTGA CATTAAATTT CTGTTATTG TTAAAAAAA AAAA AAAAAAAA AAAAAAAA	1080
	AAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAA	1123

## 45 (2) INFORMATION FOR SEQ ID NO: 16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 890 base pairs
- (B) TYPE: nucleic acid
- 50 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

55	TTTTAATTGA TCTGTGARAA AACTTAAGAA AATCACAATT TCAGCTAACCA GCAATTGTGT	60
	CCCAAAGATG AAGATACTAT AACCTCAAAT GGTGCAGATC CAGAACTGGG CTGGATGACA	120
60	TCCCTACTGT GCCATGTCCCT GGGCATTG GAAGGGACTG GACCTCTTTC CCCTCATCAA	180

	AGGAAACAGC AGTCTTGCC TCTTCCTGTT GGTTGTGCC AAGGGCTACA GTAGCTCTGA	240
	AATAACAAGA GCTCTGTAAT AACAGTAATA AATAGCTCTG AAATAACAGT CCTAAGAACT	300
5	CCTAAAGTCC TGAGAACATT TCTTGTAATG CAGCTTTTC TCTTCCTGAG AAACAGTGTG	360
	TTCTAATGGG ATTCCCAGGC AGTTCCTACA CCTACGGTGT GTGTTCCAGC AGGGAGGAGT	420
10	TATGGGCTGG GCTGCCTTT CCCATGGTC TTCATTCCA ATGAAAGTT CACTCTGCTT	480
	AGTTTGGAAAT TATTTTCTT TCAGTTGTTG TGAAACCTTT GCTTTTTATT GATTTATACA	540
	ATACAATTGG TGGGAGGGTG GACTTGGGAT GGGAGTGGGA AAAGCATGTA AGAGCTCCTT	600
15	TTGTGATGGT CCATCTACCC AAAAGAGATC TGCTTAGTG AACGATACTC TTTCATTTTT	660
	CTAAATTAGA TCAAGTTGTT ATTGATTITA GATGACTTGT ATGCAAATTG GAAAAACTTT	720
20	TTTTTTAAA GCTGATTGGG AACTACAAAC AATGAATGGA ATCTACTGAC ACAGCTAATT	780
	GGAAAACAGA TGTCTTCTTC TGTCCTATTG ATGCTGGTGT TTAAAAAACAA TCACTTAAA	840
	AAAAAGAATA AATAGTTCTA AAAGCAAAA AAAAAAAA AAAAAAATTC	890
25		

## (2) INFORMATION FOR SEQ ID NO: 17:

	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 619 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:	
	TCAGGCCCCG CTGACTCCGC CCCGCAACAC TCTCACTCGC CCTTCGTGTC CCATCAGGTC	60
	CCGCTGACTC CGCCCCGCAA TACTCTCACT CGCCCTTYGT GTCCCATCAG GTCCCGCTGA	120
40	CTCCGCCCCG CAACACTCTC ACTTGCCCTT CGTGTCCCAT CAGGTCTGTC TGACTCCATC	180
	TCCTCAGGGT CTCCAACATG TCCCTTCCTT GCCACCTCTT GCCTGGATTA CTACAGCAGC	240
45	TTCTAACGAG TCTCCCTGCC TTTCAGTTCT CGGCACCGCT TCAAGTTGTC AGTCTGGATG	300
	GTCTGTCACT CCCAGGCCA AAACGTGTA CGGCTTCCCT TTGCCTTCAG GACGAAGTCC	360
50	GTGCTGTCTG ACATAACTTA TAGGACCTTT TAGCCAGCCT GGGCAACATA GCAAGACCT	420
	GTCTCTACCA GAAAATACAA AAATGAGCCA GGCATAGTGG TGTGCACCTG TAGTCCCAGC	480
	TACTTGGGAG GCTGAGGTGG GAGGATCACC TGAGCCCAGG AAGTCAAGGC TGCCAGTGAG	540
55	CCATGATCAC ACCACTGCAC TCCAGCCTGG GCCACAGAGT GAGACCTGT CTCAAAAAAA	600
	AAAAAAA AAAACTCGA	619

## (2) INFORMATION FOR SEQ ID NO: 18:

## (i) SEQUENCE CHARACTERISTICS:

- 5                   (A) LENGTH: 1768 base pairs  
                  (B) TYPE: nucleic acid  
                  (C) STRANDEDNESS: double  
                  (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

10	AATTTAATAT TTTTTAGTAT TACAATATAT TCTTATAAAA AAGGTCCAAG TGAAAAAGGA	60
	CACTGTAGAT TAIGTCCATT AGCCTCATTT GTICATCTGAG GCACGCTGGTG AGAACAGCCT	120
15	TGGCTGAAGG CATCCCCGCGT AGAAAGTCGGG GGAGATAGAT AGTCACAGTT CCCCAGTTGG	180
	TGGAAATGGG ATGGGAGTAG GGAGAGGCTG GAACAGACCC TTCCCCATTC ACCTGGRRGA	240
20	ATTTTCTCCT CCCACTGCCC TAAACACTTT ATTTCCATCA CAGGGGAGAA ATGCTGCTGA	300
	GAAGGTTGIG TTGTTAGGT TGATGACGAA TTTTACATIG GCCACAAAAT TAGCTAGAGA	360
	AACTTATCTA AAGGTGGCAG GAGCAGTGGG GAGGGCATGA AGAAAGCAAG ACCAAGAAC	420
25	AACCTATTAA GGACCAGCTC AGCCACCCCG ACTGGCACCA GCCCCTTCCTT ACTCAGTTGA	480
	GTATGAGTCC ATGGTCCAAG GCACTGTTGG AGATCTGGCT ACAGTGGCAT CTAGCACCAG	540
30	AGCCACTGGC CAGATGAGA AAATAAATAG AAAAATATCT TTCTTTAGA GTGAGAAGGC	600
	TGAGCTCTGG AACAAACGTAT TTGTTGCTCTC TGTCAACAGT TGAACCAAAT TCTGCTTTTC	660
	TGAAGATCAA ATGTATCTTG AACAGCTTCC ATAGTCTTT TGTTTCCAGG TGCATGATCCA	720
35	GTCTTCCATG GTGGGTGGGA ATGCCAGACA CGCTTGTGGA GCCCTCCCT GTTCCCTGCC	780
	CCTGAGGGGG TTAGGTTGAC ATCAGCCTGG TCAGTTGGG AGAGGACCTT TAGAGGCCTC	840
40	ACCCACAACC TCCCCATCTC CCCAACACTT GTCTTGCAGT GGGAGCTCTT GGGGCTGCAG	900
	ATGCATATAG CCAAACCTCTC TGCAGCTGTT CTGCTGGAA GCCTTCATCT TGCCTCTCAC	960
	TGGGTTCCAG GATGGCCTCT TCACACCTGT GTCAAGCCAGG CTTGCACTTG CTCAGATCCC	1020
45	TCCCCACCAGA ACACACACAC ACCGCCCCCC CCCCTCAAACC AACGGCACATG CTGGGCTCAC	1080
	CGACCCCTGTG TTCTTCCCCC CCCGCAGCTA CTACGGTCCC AGCCCCAGGA GTTGGATGCA	1140
	AGTGAAAGGC AGAAGATAGG CAGCTGAGAG TAGGCCAGC TCACCACTCT CCACATGGCAA	1200
50	TAACCCCTGAG CCAGGGATTA GGTTGGAAAG TGAGAAACAC AGGGAAAGGGC AGAAGGGCCA	1260
	AGAGCTCATT GATGGTAGAG GTTGNCAAGG GCCAGTCTCA AAGAAGATGA AAGGCCAACT	1320
55	CGGAACGTGG TATTGAATAA GAGCCTTGAT GGAGTTTAG AAAAATTTG TCTAGATACA	1380
	GCCATCCCAT CCACCAAGGC CAGCATGAGA TGGACAAAAT GGAAGGTGGC AGTGGATGGG	1440
60	AGGACCAGAA GGAACCCCTT GCAAGTTGGG CTGAAGAACCCAAATGGTA CCARAAATGG	1500

	GTGKCCCCCC TCTCAGCCMT CCTCCTTGGC ACCTTCAGGT GATGTGCTCC CCAGAGGATA	1560
	TCAGCCTTCC TCCCTCATCC CCATCTCCCC AGTTTCCCTT GCCTGCTCTG CTGTCGCAC	1620
5	CATCTGAACG CCTGAGAGGA GGGGCCACCC TTAGAGACAG CATGTTAATG TAGAGAACTA	1680
	TGGGATGGAG CTAAGCAITC AAGTGCIGCC CTCTGCTGAG GGGCTGTAGG GGACTCCAAG	1740
10	GCAACATTTG AGGTCACTGT CTGGCTTC	1768

## (2) INFORMATION FOR SEQ ID NO: 19:

15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1699 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:	
	CTCGTGCCGA ATT CGGCACG AGCGAAAAGA TGGCGGTCTT GGCACCTCTA ATT GCTCTCG	60
25	TGTATTCCGT GCCCGCAGCTT TCACGATGGC TCGCCCAACC TTACTACCTT CTGTCGGCCC	120
	TGCTCTCTGC TGCCCTCCTA CTCGTGAGGA AACTGCCGCC GCTCTGCCAC GGTCTGCCA	180
30	CCCAACGCGA AGACGGTAAC CCGTGTGACT TTGACTGGAG AGAAGTGGAG ATCCTGATGT	240
	TTCTCAGTGC CATTGTGATG ATGAAGAACC GCAGATCCAT CACTGTGGAG CAACATATAG	300
	GCAACATTTT CATGTTTAGT AAAGTGGCCA ACACAATTCT TTCTTCCGC TTGGATATTC	360
35	GCATGGGCCT ACTTTACATC ACACTCTGCA TAGTGTCCCT GATGACGTGC AAACCCCCC	420
	TATATATGGG CCCTGAGTAT ATCAAGTACT TCAATGATAA AACCAATTGAT GAGGAACCTAG	480
40	AACGGGACAA GAGGGTCACT TGGATTGTGG AGTTCTTTGC CAAATTGGTCT AATGACTGCC	540
	AATCAATTGCG CCCATATCTAT GCTGACCTCT CCCTAAATA CAACTGTACA GGGCTAAATT	600
	TTGGGAAGGT GGATGTTGGA CGCTATACTG ATGTTAGTAC GCGGTACAAA GTGAGCACAT	660
45	CACCCCTCAC CAAGCAACTC CCTACCTGTA TCCCTTTCCA AGGTGGCAAG GAGGCAATGC	720
	GGCGGCCACA GATTGACAAG AAAGGACGGG CTGTCTCATG GACCTTCTCT GAGGAGAATG	780
	TGATCCGAGA ATTAACTTA AATGAGCTAT ACCAGCGGGC CAAGAAACTA TCAAAGGCTG	840
50	GAGACAATAT CCCTGAGGAG CAGCCTGTGG NTTCAACCCC CACCAAGTG TCAGATGGGG	900
	AAAACAAGAA GGATAAATAA GATCCTCACT TTGGCAGTGC TTCCTCTCT GTCAATTCCA	960
55	GGCTCTTTCC ATAACCACAA GCCTGAGGCT GCAGCTTTT ATTATGTTT TCCCTTTGGC	1020
	TGTGACTGGG TGGGGCAGCA TGCAGCTCT GATTTAAAG AGGCATCTAG GGAATTGTCA	1080
60	GGCACCCCTAC AGGAAGGCCT GCCATGCTGT GGCCAACGTG TTCACTGGAG CAAGAAAGAG	1140

	ATCTCATAGG ACGGAGGGGG AAATGGTTTC CCTCCAAGCT TGGGTAGTG TGTTAACTGC	1200
	TTATCAGCTA TTCAGACATC TCCATGGTTT CTCCATGAAA CTCTGTGGTT TCATCATTCC	1260
5	TCTCTAGTTG ACCTGCACAG CTTGGTTAGA CCTAGATTTA ACCCTAAGGT AAGATGCTGG	1320
	GGTATAGAAC GCTAAGAATT TTCCCCCAAG GACTCTTGCT TCCTTAAGCC CTTCTGGCTT	1380
10	CGTTTATGGT CTTCATTAAA AGTATAAGCC TAACTTTGTC GCTAGTCCTA AGGAGAAACC	1440
	TTTAACCACA AAGTTTTTAT CATTGAAGAC AATATTGAAC AACCCCTAT TTGTGGGGA	1500
	TTGAGAAGGG GTGAATAGAG GCTTGAGACT TTCTTGTG TGTTAGGACT TGGAGGAGAA	1560
15	ATCCCCCTGGA CTTCACTAA CCCTCTGACA TACTCCCCAC ACCCAGTTGA TGGCTTTCCG	1620
	TAATAAAAAG ATTGGGATTT CCTTTGAAA AAAAAAAA AAAAAAAA AAAAAAAA	1680
20	AAAAAAAAAA AAAAAAAAG	1699

## (2) INFORMATION FOR SEQ ID NO: 20:

25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 736 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:	
	AAGTGAGTTA AGGACGTACT CGTCTTGGTG AGAGCGTGAC TGCTGAGATT TGGGAGTCTG	60
35	CGCTAGGCCCG CTTGGAGTT CTGAGCCGAT CGAAGAGTTC ACTCATGTTT GCACCCCGGG	120
	TGATCCGTGC TTTTCGAAG AACAGACTC TCGGCTATGG AGTCCCCATG TTGTTGCTGA	180
40	TTGTTGGAGG TTCTTTGGT CTTCGTGAGT TTTCTCAAAT CCGATATGAT GCTGTGAAGA	240
	GTAAAATGGA TCCTGAGCTT GAAAAAAAC TGAAAGAGAA TAAAATATCT TTAGAGTCGG	300
	AATATGAGAA AATCAAAGAC TCCAAGTTG ATGACTGGAA GAATATTGCA GGACCCAGGC	360
45	CTTGGGAAGA TCCGTACCTC CTCCAAGGAA GAAATCCAGA AAGCCTTAAG ACTAAGACAA	420
	CTTGACTCTG CTGATTCTTT TTTCTTTTTT TTTTTTTTA AATAAAAATA CTATTAAC TG	480
	GACTTCCTAA TATATACTTC TATCAAGTGG AAAGGAAATT CCAGGCCAT GGAAACTTGG	540
50	ATATGGTAA TTTGATGACA AATAATCTTC ACTAAAGGTC ATGTACAGGT TTTTATACTT	600
	CCCAGCTATT CCATCTGTGG ATGAAAGTAA CAATGTGGC CACGTATATT TTACACCTCG	660
55	AAATAAAAAT TGTGAATACT GCTCCAAAAA AAAAAAAAGT NGCGAGCTT TCCCTAGGGG	720
	GGTAATTNGC TGNIGC	736

## (2) INFORMATION FOR SEQ ID NO: 21:

## (i) SEQUENCE CHARACTERISTICS:

- 5                   (A) LENGTH: 1688 base pairs  
                  (B) TYPE: nucleic acid  
                  (C) STRANDEDNESS: double  
                  (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

10	CAAAGAAGGG ATTCACTTTC CATTGGTGGA GCTGCTGAAA AATTAAACCA AGTACCCCTAC	60
	TGATAGGGAC TCCATATGGA AGTGCTTGAA GTTICTGGGA AGTCGGCATC CAACCCTGGT	120
15	GCTTCCCTTG GTGCCAGAGC TTCTGAGCAC CCACCCATT TTGACACAG CTGAACCAGA	180
	CATGGATGAT CCAGCTTATA TTGCAGTTTT GGTAATTATT TTCAATGCTG CTAAAACCTG	240
20	TCCAACAATG CCAGCATTGT TCTCAGATCA CACCTTCAGG CACTATGCCT ACCTCCGAGA	300
	CAGTCCTTCT CATCTTGTTC CTGCCTTGAG GTTACCAAGGT AGAAAACCTGG TGTCATCAGC	360
	TGTTTCTCCC AGCATCATACTC CAAGAGAGGA TCCTTCCAG CAGTCCTGC AGCAGAGCCT	420
25	TGAAAGAGTG TATAGTCTTC AGCACTTGGA CCCTCAGGGGA GCCCAGGAGC TGCTGGAATT	480
	CACCATCAGG GATCTGCAAA GACTTGGAGA ACTTCAATCT GAATTGGCAG GAGTAGCTGA	540
	TTTCTCTGCC ACCTATCTTC GCTGTCAACT ACTTCTCATC AAGGCCCTGC AGGAAAAGTT	600
30	GTGGAATGTA GCTGCCCTT TGTATTGAA GCAGAGTGAT TTGGCCTCAG CAGCAGCAGA	660
	ACAGATTATG GAAGAGACCT ACAAAATGGA ATTCAATGTAC AGTGGTGTGG AGAATAAGCA	720
35	GGTGGTGATT ATACATCACA TGAGGCTGCA GGCCAAAGCT TTGCAACTTA TAGAACAGC	780
	ACGAACATACA CGAGGACTTG ACCCCATTATT TGGGATGTGT GAAAAATTATT TACAGGAAGT	840
40	AGACTTTTTT CAGAGGTATT TCATCGCTGA TTTGCCAC TTGCAGGACA GCTTTGTGGA	900
	CAAACCTCTT GACCTTATGC CCCGACTCAT GACATCCAAA CCTGCAGAAG TGTCAAAAT	960
	TCTACAGACC ATGCTGCGAC AGAGTGCCTT TCTGCATCTC CCGCTTCCAG AGCAGATCCA	1020
45	CAAAGCCTCA GCCACCATCA TCGAGCCAGC GGGCGAGTTC AGACAACCCCT TTGCGGTTTA	1080
	CCTCTGGGTT GGTGGTTGCC CTGGGATGTGATGCAACCC TGGAGCATGT GCAGGATCCT	1140
	CAGAACACTG TTAAGGTCCA GGGCTTATA TCCAGATGGC CAGGTTTCAG ATGATTCAACC	1200
50	CCAAGCCTGC AGACTTCCGG AATCCTGCC CAGGGCGCA CCGGCTCATC ACTCAGGTTT	1260
	ATCTCTCCCCA CACCGCTTGG ACAGAGGCAT GCCAGGTGGA AGTGAGGCTG CTGCTGGCCT	1320
55	ACAAACTCCAG TGCTCGCATT CCAAAATGCC CCTGGATGGA GGGTGGTGAG ATGTCACCAC	1380
	AGGTGGAAAC CAGCATCGAG GGCACCATTC CCTTCAGCAA GCCTGTAAAA GTTTATATAA	1440
60	TGCCCAAACC TGCACGGCGC TAAGGAAAAA ACAGTCTTCC CAACCGTGCC TAGAGGGCCC	1500

	TTCTTAGGTG TCAGAACATGAG CCAAGCCTGA AGCACTTCAC CTGGAATTGA TGTGTAGGCT	1560
	TAAGGAGTAT GTGACCCCTTA CAGTCTCATC TGGTATCAAACACAGGATAA ATTGTTTCCTT	1620
5	CATTAACAAAAA TAAAAAAACCT TCAAGTCTAC TTACCCCTCT CCTGTCCACA ATAAAGTTGA	1680
	GAAAACAC	1688

10

(2) INFORMATION FOR SEQ ID NO: 22:

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 2045 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:	
20	GAGCTCTCGG GGTATCGAGG AGGCAGGCC GCGGGCGCAC GGGCGAGCGG GCCGGGAGCC	60
	GGAGCGGCGG AGGAGCCGGC AGCACCGGCG CGGCGRGCTC CAGGGGAGGC GGTCGACGCT	120
25	CCTGAAACT TGCGCGCGCG CTCGCCCCACT GCGCCCCGGAG CGATGAAGAT GGTCGCGCCC	180
	TGGACGCGGT TCTACTCCAA CAGCTGCTGC TTGTGCTGCC ATGTCGGCAC CGGCACCATC	240
30	CTGCTCGCGC TCTGGTATCT GATCATCAAT GCTGTGGTAC TGTTGATTTTG ATTGAGTGCC	300
	CTGGCTGATC CGGATCAGTA TAACTTTCA AGTTCTGAAC TGGGAGGTGA CTTTGAGTTC	360
	ATGGATGATG CCAACATGTG CATTGCCATT GCGATTTCTC TTCTCATGAT CCTGATATGT	420
35	GCTATGGCTA CTTACGGAGC GTACAAGCAA CGCGCAGCTG GGATCATCCC ATTCTCTGT	480
	TACCAAGATCT TTGACTTTGC CCTGAACATG TTGGTTGCAA TCACTGTGCT TATTTATCCA	540
40	AACTCCATTG AGGAATACAT ACGGCAACTG CCTCCTAATT TTCCCTACAG AGATGATGTC	600
	ATGTGCAGTG AATCCTACCT GTTTGGTCCT TATTATCTT CTGTTTATTA GCATTATCTT	660
	GACTTTAAG GGTTACTTGA TTAGCTGTGT TTGGAACTGC TACCGATACA TCAATGGTAG	720
45	GAACCTCTCT GATGTCTCTGG TTATATGTAC CAGCAATGAC ACTACGGTGC TGCTACCCCC	780
	GTATGATGAT GCCACTGTGA ATGGTGCTGC CAAGGAGCCA CCGCCACCTT ACCTGTCTGC	840
50	CTAAGCCTTC AAGTGGGCGG ACTGAGGGCA GCAGCTTGAC TTTGCAGACA TCTGAGCAAT	900
	AGTTCTGTTA TTTCACCTTTT GCCATGAGCC TCTCTGAGCT TGTTTGTGTC TGAAATGCTA	960
	CTTTTTAAAAA TTTAGATGTT AGATTGAAAA CTGTAGTTT CAACATATGC TTTGCTRGAA	1020
55	CACTGTGATA GATTAACGTG AGAATTCTTC CTGTACGATT GGGGATATAA YGGGCTTCAC	1080
	TAACCTTCCCC TAGGCATTGA AACCTCCCCC AAATCTGATG GACCTAGAAG TCTGCTTTTG	1140
60	TACCTGCTGG GCCCCAAAGT TGGGCATTTT TCTCTCTGTT CCCTCTCTTT TGAAAATGTA	1200

	AAATAAAACC AAAAATAGAC AACTTTTCT TCAGCCATTC CAGCATAGAG AACAAAACCT	1260
	TATGGAAACA GGAATGTCAA TTGTGTAATC ATTGTTCTAA TTAGGTAAAT AGAAGTCCTT	1320
5	ATGTATGTGT TACAAGAATT TCCCCCACAA CATCCTTTAT GACTGAAGTT CAATGACAGT	1380
	TIGTGTGTTGG TGGTAAAGGA TTTTCTCCAT GGCTGAAATT AAGACCATTA GAAAGCACCA	1440
10	GGCCGTGGGA GCAGTGACCA TCTGCTGACT GTTCTTGTGG ATCTTGTGTC CAGGGACATG	1500
	GGGTGACATG CCTCGTATGT GTTAGAGGGT GGAATGGATG TGTTTGGCGC TGCATGGGAT	1560
	CTGGTGCCCC TCTTCTCCTG GATTACATC CCCACCCAGG GCCCGCTTTT ACTAAGTGTT	1620
15	CTGCCCTAGA TTGGTTCAAG GAGGTCATCC AACTGACTTT ATCAAGTGGA ATTGGGATAT	1680
	ATTTGATATA CTTCTGCCTA ACAACATGGA AAAGGGTTTT CTCTTCCCTG CAAGCTACAT	1740
	CCTACTGCTT TGAACCTCCA AGTATGTCTA GTCACCTTTT AAAATGTAAC CATTTCAGA	1800
20	AAAATGAGGA TTGCCCTCCCT TGTATGCGCT TTTTACCTTG ACTACCTGAA TTGCAAGGGA	1860
	TTTTATATA TTCATATGTT ACAAAAGTCAG CAACTCTCCT GTGTTTCAT TATTGAATGT	1920
25	GCTGTAAATT AAGTYGTTG CAATAAAAC AAGGTTGCC CACATCCAAA AAAAAAAA	1980
	AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAAN	2040
30	NAAAAA	2045

(2) INFORMATION FOR SEQ ID NO: 23:

35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1101 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
40	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:	
45	TTGTTTGCCT ACCGTCAATA TTCCCGGCC TGGACGGTTA AATAGCTAAA GCTGGCGCGG	60
	GGCTGTCACC TCCGCCTCTG CTCCCCGACC CGGCCATGCG CGGCCTCGGG CTCTGGCTGC	120
	TGGGCGCGAT GATGCTGCCT GCGATTGCC CCAGCCGGCC CTGGGCCCTC ATGGAGCAGT	180
50	ATGAGGTCGT GTTGCCTGYGG CGTCTGCCAG GCCCCGAGT CGGCCGAGCT CTGCCCTCCC	240
	ACTTGGGCCT GCACCCAGAG AGGGTGAGCT ACgtccttgg GGCCACAGGG CACAACCTCA	300
	CCCTCCACCT GCGGAAGAAC AGGGACCTGC TGGGYTCCGG CTACACAGAG ACCTATAACGG	360
55	CTGCCAATGG CTCCGAGGTG ACGGAGCAGC CTGGCGGGCA GGACCACTGC TTYTACCAAGG	420
	GCCACAGTAGA GGGGTACCCG GACTCAGCCG CCAGCCTCAG CACCTGTGCC GGCCCTCAGGG	480
60	GTTCCTTCCA GGTGGGGTCA GACCTGCACC TGATCGAGCC CCTGGATGAA GGTGGCGAGG	540

	GGGGACGGCA CGCCGTGTAC CAGGCTGAGC ACCTGCTGCA GACGGCCGGG ACCTGCGGGG	600
5	TCAGCGACGA CAGCCTGGGC AGCCTCTGG GACCCCGAC GGCAGCCGTC TTCAGGCCTC	660
	GGCCCGGGGA CTCTCTGCCA TCCCGAGAGA CCCGCTACGT GGAGCTGTAT GTGGTCTGG	720
	ACAATGCAGA GTTCCAGATG CTGGGGAGCG AAGCAGCCGT GCGTCATCGG GTGCTGGAGG	780
10	TGGTGAATCA CGTGGACAAG CTATATCAGA AACTCAACTT CCGTGTGGTC CTGGTGGCC	840
	TGGAGATTTG GAATAGTCAG GACAGGTTCC ACGTCAGCCC CGACCCCCAGT GTCACACTGG	900
15	AGAACCTCCT GACCTGGCAR GCACGGCAAC GGACACGGCG GCACCTGCAT GACAACGTAC	960
	AGCTCATCAC GGGTGTCGAC TTCAACGGGA CTACTGTGGG GTTTGCCAGG GTGTCCACCA	1020
	TGTGCTCCCA CAGCTCAGGG GCTGTGAACC AGGACCACAG CAAGAACCCC GTGGGCGTGG	1080
20	CCTGCACCAT GGCCCATGAG A	1101

## 25 (2) INFORMATION FOR SEQ ID NO: 24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1659 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

35	CCGGGCTGCA GGATTCTGGCA CGAGGTGGGA GCCAAGAAGA AAGGTTTGCT CCCGGGTGGA	60
	ACAGGGATTA TCCTCCTCCT CCCCTTAAGA GTCATGCTCA AGAGAGACAC TCTGGCAACT	120
40	TTCCTGGCAG AGATTCACTT CCCTTTGATT TCCAGGGCA TTCCGGGCCT CCTTTGCAA	180
	ATGTAGAGGA GCATTCTTC AGCTATGGAG CTAGAGACGG ACCGCATGGT GACTATCGAG	240
	GAGGGGAGGG ACCTGGACAT GATTTCAGGG GGGGAGATT TTCTGTCTTCT GATTTCAGA	300
45	GCAGAGATTG ATCACAGTTG GACTTCAGGG GTAGGGACAT ACATTCTGGG GATTTTCGGG	360
	ATAGAGAAGG ACCACCTATG GACTATAGGG GTGGAGATGG TACTTCTATG GATTATAGAG	420
50	GTAGGGAGGC ACCTCATATG AACTACAGAG ACAGGGATGC TCACGCTGTT GACTTCAGAG	480
	GTAGGGATGC TCCTCCATCT GACTTCAGGG GCCGGGGCAC TTATGATTTA GATTTTAGAG	540
	GCCGGGATGG ATCCCATGCA GATTTTAGGG GAAGGGATTG ATCAGATTG GATTTAGGG	600
55	CCAGAGAACCA GTCCCGTTCT GATTTAGGA ATAGAGATGT ATCTGATTTG GACTTTAGAG	660
	ACAAAGACGG AACACAAGTA GACTTTAGAG GCCGAGGTTTC AGGTACTACT GATCTAGACT	720
60	TTAGGGACAG GGATAACGCCA CATTCAAGATT TCAGAGGTAG ACACCGATCT AGGACTGATC	780

	AGGATTTTAG GGGCAGAGAG ATGGGATCTT GTATGGAATT TAAAGATAGG GAGATGCC	840
	CTGTGGATCC AAATATTTTG GATTACATTC AGCCCTCTAC ACAAGATAGA GAACATTCTG	900
5	GTATGAATGT GAACAGGAGA GAAGAATCCA CACATGACCA TACGATAGAA AGGCCTGCTT	960
	TTGGCATTCA GAAGGGAGAA TTTGAGCATT CAGAAACAAG AGAAGGAGAA ACACAAGGTG	1020
10	TAGCCTTTGA ACATGAGTCT CCAGCAGACT TTCAGAACAG CCAAAGTCCA GPTCAAGACC	1080
	AAGATAAGTC ACAGCTTTCT GGACGTGAAG ACCAGAGTTC AGATGCTGGT CTGTTAAAG	1140
	AAGAAGGCGG TCTGGACTTT CTTGGGCGGC AAGACACCGA TTACAGAACG ATGGAGTACC	1200
15	GTGATGTGGA TCATAGGCTG CCAGGAAGCC AGATGTTGG CTATGCCAG AGCAAGTCTT	1260
	TTCCAGAGGG CAAAAGTGCC CGAGATGCC AACGGGACCT TCAGGATCAA GATTATAGGA	1320
20	CCGGCCCAAG TGAGGAGAAA CCCAGCAGGC TTATTGCAATT AAGTGGGTA CCTGAAGATG	1380
	CCACAAAAGA AGAGATTCTT AATGCTTTTC GGACTCCTGA TGGCATGCCCT GTAAAGAATT	1440
	GCAGTTGAAG GAGTATAACA CAGGTTACGA CTATGGCTAT GTCTCGTGG AGTTTCACT	1500
25	CTTGGAAAGAT GCCATCGGAT GCATGGAGGC CAACCAGGCT GGTGATTAGT AACTAAAGCA	1560
	TATGCTGTGG AACATCCAGC ACTGATGCCA GATTACCTGT CCCTAATACT GAGCAGAACG	1620
30	TGGTGAATGA AACAGGAGAT CCCTCAGTCA AAACAAAAA	1659

(2) INFORMATION FOR SEQ ID NO: 25:

35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1329 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:	
45	TCTGTTCTC TCTCCTGGAA GCTTGCAGAC CTCCCTTCAG AACCAATCCC AAGAAGCCAC	60
	CTATCCGGAA CAACACAAGG ATGCTGCCG ACTGGAAGAG STCCTTGATC CTCATGGCTT	120
	ACATCATCAT CTTCTCACT GGCTCCCTG CCAACCTCCT GGCCCTGCCG GCCTTGTGG	180
50	GGCGGATCCG CCAGCCCCAG CCTGCACCTG TGCACTCCT CCTGCTGAGC CTGACGCTGG	240
	CCGACCTCCT CCTGCTGCTG CTGCTGCCCT TCAAGATCAT CGAGGCTGCCG TCGAACTTCC	300
	GCTGGTACCT GCCCAAGGTC GTCTGCCGCC TCACGGATTT TGGSTTCTAC AGCAGCATCT	360
55	ACTGCAGCAC GTGGCTCCTG CGGGGCATCA GCATCGAGCG CTACCTGGGA GTGGCTTTCC	420
	CCGTCCAGTA CAAGCTCTCC CGCCGGCCTC TGTATGGAGT GATTGCAAGCT CTGGTGGCCT	480
60	GGGTTATGTC CTTTGGTCAC TGCACCATCG TGATCATCGN TCAATACTTG AACACGACTG	540

	AGCAGGTCAG AAGTGGCAAT GAAATTACCT GCTACGAGAA CTTCACCGAT AACCAAGTTGG	600
5	ACGTGGTGCT GCCCGTGMGG STGGAGCTGT GCCTGGTGCT CTTCTTCATS CCCATGGCAG	660
	TCACCACATCTT CTGCTACTGG CGTTTGTGT GGATCATGCT CTCCCCAGCCC CTTGTGGGG	720
	CCCAAGAGGCG GCGCCGAGCC GTGGGGCTGG CTGTGGTGAC GCTGCTCAAT TTCCCTGGTGT	780
10	GCTTCGGACC TTACAACGTG TCCCACCTGG TGGGGTATCA CCAGAGAAAA AGCCCCCTGGT	840
	GGCGGTCAAT AGCCGTGKIG TTCAGTTAC TCAACCCAG TCTGGACCCC CTGCTCTTCT	900
15	ATTTCTCTTC TTCAGTGGTG CGCAGGGCAT TTGGGAGAGG GCTGCAGGTG CTGCGGAATC	960
	AGGGCTCCTC CCTGTTGGGA CGCAGAGGCA AAGACACAGC AGAGGGGACA AATGAGGACA	1020
	GGGGTGTGGG TCAAGGAGAA GGGATGCCA GTTCGGACTT CACTACAGAG TAGCAGTTTC	1080
20	CCTGGACCTT CAGACGTGCG CTGGGTTACA CAGGACCTGG GAAGCCTGGG AGAGGCGGAN	1140
	CAGGAAGGCT CCCATCCAGA TTCAGAAATC CTTAGACCCA GCCCAGGACT GCGACTTTGA	1200
25	AAAAAAATGCC TTTCACCAGC TTGGTATCCC TTCTGACTG AATTGTCCTA CTCAAAGGAG	1260
	CATAAGTCAG AGATGCACGA AGAAGTAGTT AGGTATAGAA GCACCTGCGG GGTGTGGTGG	1320
	CTCATGCCT	1329
30		

## (2) INFORMATION FOR SEQ ID NO: 26:

35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 700 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:	
	GGCAGAGAGC ACCATCTGTC ATGGCGGCTG GGCTGTTGG TTTGAGCGCT CGCCGTCTTT	60
45	TGGCGGCAGC GGCGACGCGA NGGGCTCCCG GCGCCCGCG TCCGCTGGGA ATCTAGCTTC	120
	TCCAGGACTG TGGTCGCCCG GTCCGCTGTG GCGGRAAACG GCCCCCCAGA ACCGACCACAA	180
50	CCGTGGCAAG AGGACCCAGA ACCCGAGGAC GAAAACCTGT ATGAGAAGAA CCCAGACTCC	240
	CATGGTTATG ACAAGGACCC CGTTTTGGAC GTCTGGAACA TGCGACTTGT CTTCTTCTTT	300
	GGCGTCTCCA TCATCCTGGT CCTTGGCAGC ACCTTTGTGG CCTATCTGCC TGACTACAGG	360
55	TGCCACAGGGT GTCCAAGAGC GTGGGATGGG ATGAAAGAGT GGTCCCGCCG CGAAGCTGAG	420
	AGGCTTGTGA AATACCGAGA GGCAATGGC CTTCCCATCA TGGAATCCAA CTGCTTCGAC	480
60	CCCAGCAAGA TCCAGCTGCC AGAGGATGAG TGACCAGTTG CTAAGTGGGG CTCAAGAAGC	540

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ACCGCCTTCC CCACCCCTG CCTGCCATTC TGACCTCTTC TCAGAGCACC TAATTAAAGG	600
GGCTGAAAGT CTGAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAANA	660
5 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA ANGGGGGGN	700

## (2) INFORMATION FOR SEQ ID NO: 27:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

20 GGCACGAGCT CCACTCGGTT TCTCTCTTG CAGGAGCACC GGCAGCACCA GTGTGTGAGG	60
GGAGCAGGCA GCGGTCTTAG CCAGTTCTT GATCCTGCCA GACCACCCAG CCCCTGGCAC	120
AGAGCTGCTC CACAGGCACC ATGAGGATCA TGCTGCTATT CACAGCCATC CTGGCCTTCA	180
25 GCCTAGCTCA GAGCTTTGGG GCTGTCGTGA AGGAGCCACA GGAGGGAGGTG GTTCCTGGCG	240
GGGGCCGCAG CAAGAGGGAT CCAGATCTCT ACCAGCTGCT CCAGAGACTC TTCAAAAGCC	300
30 ACTCATCTCT GGAGGGATTG CTCAAAGCCC TGAGCCAGGC TAGCACAGAT CCTAAGGAAT	360
CAACATCTCC CGAGAACGT GACATGCATG ACTTCTTTGT GGGACTTATG GGCAAGAGGA	420
GGTCCAGCC AGACTCTCC ACAGGATGTGA ATCAAGAGAA CGTCCCCAGC TTTGGCATCC	480
35 TCAAGTATCC CCCGAGAGCA GAATAGGTAC TCCACTTCG GACTCCTGGA CTGCATTAGG	540
AAGACCTCTT TCCCTGTCCC AATCCCCAGG TCGCAGCAGCT CCTGTTACCC TTTCTCTTCC	600
40 CTGTTCTTGT AACATTCTTG TGCTTTGACT CCTTCTCCAT CTTTCTTACCC TGACCCCTGGT	660
GTGGAAACTG CATACTGAAT ATCCCCAACC CCAATGGCA TTGACTGTAG AATACCCCTAG	720
AGTTCCCTGTA GTGTCCTACA TTAAAAATAT AATGTCTCTC TCTATTCCCTC AACAAATAAAG	780
45 GATTTTGCA TATGAAAAAA AAAAAAAAAA AAAAAAAAAA NAAANAAAAA AA	832

## (2) INFORMATION FOR SEQ ID NO: 28:

50

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 55 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

60 GGCACGAGGC TCCCTAACCGG GTTGTACCCG CTGGAGACGG TTGGGAGAAC CGTTGTGGCG	60
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130

	ACGGCTACAC GAGGCAAACG ACTTCTCCCT TCTTTGAACG GGACCCCGCG ACCACCAGAG	120
	TCGGCGTAAC TATCGCCTGA CAGGCATTAA AATCAAACGG TATTGAGATG GATTGGGTTA	180
5	TGAAACATAA TGGTCCAAT GACGCTATGA TGGGACAGTA CGACTTCGTG GACTACCATT	240
	TGGTTGCAGC AAAGAGGAAA TAGTTCAGIT CTTCAGGG TTGGAATCG TGCCAATGGG	300
10	ATAAACATTGA CGATGGACTA CCAGGGAGA AGCACAGGG AGGCCTTCGT GCAGTTTGCT	360
	TCAAAAGGAGA TAGCAGAAAA TGCTCTGGG AACACACAAGG AAAAGAATAGG GCACAGGTAT	420
	ATTGAGATCT TCAGAAGTAG CAGGAGTGAA ATCAAAGGAT TTTATGATCC ACCAAGAAGA	480
15	TTGCTGGGAC ACCGACCGGG ACCATATGAT AGACCAATAG GAGGAAGAGG GGGTTATTAT	540
	GGAGCTGGGC GTGGAAGTAT GTATGACAGA ATGCGACGAG GAGGTGATGG ATATGATGGT	600
20	GGTTATGGAG GTTTGATGA CTATGGTGGC TATAATAATT ACGGCTATGG GAATGATGGC	660
	TTTGATGACA GAATGAGAGA TGGAAGAGGT ATGGGAGGAC ATGGCTATGG TGGAGCTGGT	720
	GATGCAAGTT CAGGTTTCAT TGGTGGTCAT TTCTGACATA TGAGAGGGTT GCCTTTCGT	780
25	GCAACTGAAA ATGACATTGC TAATTTCTTC TCACCACTAA ATCCAATACG AGTTCATATT	840
	GATATTGGAG CTGATGGCAG AGCACAGGG AGCAGATGT AGAGTTGTG ACACATGAAG	900
30	ATGCAGTAGC TGCCATGTCT AAAGATAAAA ATAACATGCA ACATCGATAT ATTGAACCT	960
	TCTTGAATTTC TACTCCTGGA GGCGCTCTG GCATGGGAGG TTCTGGAATG GGAGGCTACG	1020
	GAAGAGATGG AATGGATAAT CAGGGAGGCT ATGGATCAGT TGGAAAGAATG GGAATGGGA	1080
35	ACAATTACAG TGGAGGATAT GGTACTCCTG ATGGTTGGG TGGTTATGGC CGTGGTGGTG	1140
	GAGGCAGTGG AGGTTACTAT GGGCAAGGCG GCATGAGTGG AGGTGGATGG CGTGGGATGT	1200
40	ACTGAAAGCA AAAACACCAA CATAACAAGTC TTGACAACAG CATCTGGTCT ACTAGACTTT	1260
	CTTACAGATT TAATTTCTTT TGTATTTTAA GAACTTTATA ATGACTGAAG GAATGTGTTT	1320
	TCAAAATATT ATTTGGTAAA GCAACAGATT GTGATGGGAA AATGTTTTCT GTAGGTTTAT	1380
45	TTGTTGCATA CTTTGACTTA AAAATAAATT TTTATATTCA AACCACTGAT TTGATACTTT	1440
	TTTATATACT AGTTACTCCT AAAGATGTGC TGCCTTCATA AGATTTGGGT TGATGTATTT	1500
50	TACTATTAGT TCTACAAGAA GTAGTGTGGT GTAATTCTAG AGGATAATGG TTCACCTCTG	1560
	CGTAAACTGC AAGTCTTAAG CAGACATCTG GAATAGAGCT TGACAAATAA TTAGTGTAAAC	1620
	TTTTTCTTT AGTTCCCTCT GGACAACACT GTAAATATAA AGCCTAAAGA TGAAGTGGCT	1680
55	TCAGGAGTAT AAATTCAGCT AATTATTTCT ATATTATTAT TTTTCAAATG TCATTTATCA	1740
	GGCATAGCTC TGAAACATTG ATGATCTAAG AGGTATTGAT TTCTGAATAT TCATAATTGT	1800
60	GTACCTGGG TATGAGAGTG TTGGAAGCTG AATTCTAGCC CTAGATTTG GAGTAAAACC	1860

	CCTTCAGCAC TTGACCGAAA TACCAAAAT GTCTCCAAA AATTGATAGT TGCAGGTTAT	1920
	CGCAAGATGT CTTAGAGTAG GGTTAAGGTT CTCAGTGACA CAAGAATTCA GTATTAAGTA	1980
5	CATAGGTATT TACTATGGAG TATAATTCTC ACAATTGTAT TTTCAGTTTT CTGCCCAATA	2040
	GAGTTTAAAT AACTGTATAA ATGATGACTT TAAAAAAATG TAAGCAACAA GTCCATGTCA	2100
10	TAGTCAATAA AAACAATCCT GCAGTTGGGT TPTGTATCTG ATCCCTGCTT GGAGTTTAG	2160
	TTTAAGAAT CTATATGTAG CAAGGAAAAG GTGCTTTTA ATTTTAATCC CTTTGATCAA	2220
	TATGGCTTTT TTCCAAATG GCTAATGGAT CAAAATGAAA CCTGTTGATG TGAATTCACT	2280
15	TATTGAACCT GTTACTTGT TTTGCCAGAA ATGTTATTTAA TAAATGTCAA TGTGGGAGAT	2340
	AATAAAAAAA AAAAAAAAAA N	2361

20

(2) INFORMATION FOR SEQ ID NO: 29:

	(i) SEQUENCE CHARACTERISTICS:	
25	(A) LENGTH: 879 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:	
30	GGAATCTGCA CCATGCCCTG GGTTCTGCTC CTCCCTGACCC TCCTCACTCA CTCTGCAGTG	60
	TCAGTGGTCC AGGCAGGGCT GACTCAGCCC CCCTCGGTGT CCAAGGACTT GAGACAGACC	120
35	GCCACACTCA CCTGCACCGG GAACAACAAC AATGTTGGCG ACCAAGGAGC AGCTTGGCTG	180
	CAGCAGCACC AGGGCCACCC TCCCAAACTC CTGTCCTACA GGAATAATAA CCGGCCCTCA	240
40	GGGATCTCAG AGAGATTATC TGCATCCAGG TCAGGAGCCA CATCCTCCCT GACCATTACT	300
	GGACTCCAGC CTGAGGACGA GGCTGACTAT TACTGCGAG CATATGACAG CAGCCTCGCA	360
	GTTTGGATGT TCGGCGGAGG GACCAAGCTG ACCGTCCTAG GTCAGCCCAA GGCTGCCCTC	420
45	TCCGTCACTC TGTTCCCACC CTCCCTGAG GAGCTTCAAG CCAACAAGGC CACACTGGTG	480
	TGTCTCATAA GTGACTTCTA CCCGGGAGCC GTGACAGTGG CCTGGAAGGC AGATAGCAGC	540
	CCCGTCAAGG CGGGAGTGGG GACCACCAACA CCCTCCAAAC AGAGCAACAA CAAGTACGCG	600
50	GCCAGCAGCT ACCTGAGCCT GACGCCCTGAG CAGTGGAAAGT CCCACAGAAG CTACAGCTGC	660
	CAGGTACCGC ATGAAGGGAG CACCGTGGAG AAGACGGTGG CCCCTACAGA ATGTTCATAG	720
55	GTTCCCAACT CTAACCCCAC CCACGGGAGC CTGGAGCTGC AGGATCCCAG GGGAGGGTC	780
	TCTCTCCCCA TCCCAAGTCA TCCAGCCCTT CTCCCTGAC TCATGAAACC CCAATAATAA	840
60	TTCTCATTTGT CAATCAGAAA AAAAAAAAAA AAAAAAAAAA	879

## (2) INFORMATION FOR SEQ ID NO: 30:

## 5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## 10 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

15	GTTCCGGAGGG AAACGTGTAT TGTGGTCTCA AGMMTTGCCCA CAWATTAACC TGTGCCCTTC	60
20	AACATTCTGA TGGTGATATC TTCCGGCAAC CTGCCAACAG AGAACGCAAGA CATTCTTACC	120
25	ACCGCTCTCA CTATGATCCT CCACCAAGCC GACAGGCTGG AGGTCTGTCC CGCTTTCCIG	180
30	GGGCCAGAAG TCACCGGGGA GCTCTTATGG ATTCCCAGCA AGCATCAGGA ACCATTGTGC	240
35	AAATTGTCAAT CAATAACAAA CACAAGCATG GACAAGTGTG TGTTCATGAA GGAAAGACCT	300
40	ATTCTCATGG CGAGTCCTGG CACCCAAACC TCCGGCATT TGGCATTGTG GAGTGTGTGC	360
45	TATGTACTTG TAATGTCAAC AAGCAAGAGT GTAAGAAAAT CCACTGCCCC AATCGATACC	420
50	CCTGCAAGTA TCCTCAAAAA ATAGACGGAA AATGCTGCAA GGTGTGTCCA GAAGAACITC	480
55	CAGGCCAAAG CTTTGACAAT AAAGGCTACT TCTGGGGGA AGAAACGATG CCTGTGTATG	540
60	AGTCTGTATT CATGGAGGAT GGGGAGACAA CCAGAAAAT AGCACTGGG ACTGAGAGAC	600
	CACCTCAGGT AGAGGTCCAC GTTGGACTA TTCGAAAGGG CATTCTCCAG CACTTCCATA	660
	TTGAGAAGAT CTCCAAGAGG ATGTTTGAGG AGCTTCTCA CTTCAAGCTG GTGACCAGAA	720
	CAACCTGAG CCAGTGGAAAG ATCTTCACCG AAGGAGAAC TCAGATCAGC CAGATGTGTT	780
	CAAGTCGTGT ATGCAGAACAA GAGCTTGAAG ATTTAGTCAA GGTTTTGTAC CTGGAGAGAT	840
	CTGAAAAGGG CCACTGTGAG GCAAGACAGA CAGTATTGGA TAGGGTAAAG CAAGAAAAC	900
	CAAGCTGCAG CTGGACTGCA GGCTTATTTT GCTTAAGTCA ACAGTGCCT AAAACTCCAA	960
	ACTCAAATGC AGTCAATTAT TCACGCCATG CACAGCATAA TTGCTCCTT TGTGTGTGTG	1020
	TGTGTGTGTG TGTGTGTGTG TGTGGTAAAG GGGGGAAAGGT GTTATGCCGC TGCTCCCTCC	1080
	GTCCCCAGAGG TGGCACTGAT TCCATAATGT GGAGACTAGT AACTAGATCC TAAGGCAAAG	1140
	AGGTGTTCT CCTTCTGGAT GATTCACTCC AAAGCCTTCC CACCCAGGTG TTCTCTGAAA	1200
	GCTTAGCCTT AAGAGAACAC GCAGAGAGTT TCCCTAGATA TACTCCTGCC TCCAGGTGCT	1260
	GGGACACACC TTGCAAAAT GCTGTGGAA GCAGGAGCTG GGGAGCTGTG TTAAGTCAA	1320
	GTAGAAAACCC TCCAGTGTGTT GGTGTTGTGT AGAGAATAGG ACATAGGGTA AAGAGGCCAA	1380
		1440

	GCTGCCCTGTA GTTGTAGAG AAGAATGGAT GTGGTTCTTC TTGTGTATTG ATTTGTATCA	1500
	TAAACACTTG GAACAACAAA GACCATAAGC ATCATTTAGC AGTTGTAGCC ATTTTCTAGT	1560
5	TAACTCATGT AAACAAGTAA GAGAACATA ACAGTATTAC CCTTCACAGG TTCTCACAGG	1620
	ACATGTACCT AATTATGGTA CTTATTTATG TAGTCAGTGT ATTTCTGGAT TTTAAATTA	1680
10	ATAAAAAAAGT TAATTTGAA AAATCAAAAA AAAAAAAA AAAAAAACTC GA	1732

## (2) INFORMATION FOR SEQ ID NO: 31:

## 15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

	TTTGCAGTAC GGGCCGGATT TCCCGGGTCG ACCCACCGGT CCGCCGGAGGC TACGTGAAGA	60
25	GAGGCGCGGC GTGACTGAGC TACGGTTCTG GCTGCGTCCT AGAGGCATCC GGGGCAGTAA	120
	AACCGCTGCG ATCGCGGAGG CGGCGGCCAG GCCGAGAGGC AGGCCGGGCA GGGGTGTCGG	180
30	ACCCAGGGCG CTGGGCCGGG TTTCGGCTTC GGCCACAGCT TTTTTCTCA AGGTGCAATG	240
	AAAGCCTTCC ACACTTCTG TGTTGTCTT CTGGTGTGTTG GGAGTGTCTC TGAAGCCAAG	300
	TTTGATGATT TTGAGGATGA GGAGGACATA GTAGAGTATG ATGATAATGA CTTCGCTGAA	360
35	TTTGAGGATG TCATGGAAGA CTCTGTTACT GAATCTCCTC AACGGTCAT AATCACTGAA	420
	GATQATGAAG ATGAGACCACT TGTGGAGTTG GAAGGGCAGG ATGAAAACCA AGAAGGAGAT	480
40	TTTGAAGATG CAGATAACCA GGAGGGAGAT ACTGAGAGTG AACCATATGA TGATGAAGAA	540
	TTTGAAGGTT ATGAAGACAA ACCAGATACT TCTCTAGCA AAAATAAAGA CCCAATAACG	600
	ATTGTTGATG TTCCTGCACA CCTCCAGAAC AGCTGGGAGA GTTATTATCT AGAAATTG	660
45	ATGGTGACTG GTCTGCTTGC TTATATCATG AATTACATCA TTGGGAAGAA TAAAACAGT	720
	CGCTTGCAC AGGCCTGGTT TAACACTCAT AGGGAGCTT TGGAGAGCAA CTTTACTTTA	780
	GTGGGGGATG ATGGAACTAA CAAAGAACCC ACAAGCACAG GAAAGTTGAA CCAGGAGAAT	840
50	GAGCACATCT ATAACCTGTG GTGTTCTGGT CGAGTGTGCT GTGAGGGCAT GCTTATCCAG	900
	CTGAGGTTCC TCAAGAGACA AGACTTACTG AATGTCCTGG CCCGGATGAT GAGGCCAGTG	960
55	AGTGATCAAG TGCAAATAAA AGTAACCATG AATGATGAAG ACATGGATAC CTACGTATTT	1020
	GCTGTTGGCA CACGGAAAGC CTTGGTGCAGA CTACAGAAAG AGATGCAGGA TTTGAGTGAG	1080
60	TTTGATGAGTG ATAAACCTAA GTCTGGAGCA AAGTATGGAC TGCCGGACTC TTTGGCCATC	1140

	CTGTCAGAGA TGGGAGAAAGT CACAGACGGA ATGATGGATA CAAAGATGGT TCACTTTCTT	1200
	ACACACTATG CTGACAAGAT TGAATCTGTT CATTTTCAG ACCAGTTCTC TGGTCCAAAA	1260
5	ATTATGCAAG AGGAAGGTCA GCCTTTAAAG CTACCTGACA CTAAGAGGAC ACTGTTGTTT	1320
	ACATTTAATG TGCCCTGCTC AGGTAACACT TACCCAAAGG ATATGGAGGC ACTGCTACCC	1380
10	CTGATGAACA TGGTGATTIA TTCTATTGAT AAAGCCAAAA AGTTCCGACT CAACAGAGAA	1440
	GGCAAACAAA AAGCAGATAA GAACCGTGCC CGAGTAGAAG AGAACTTCTT GAAACTGACA	1500
	CATGTGCAAA GACAGGAAGC AGCACAGTCT CGGCGGGAGG AGAAAAAAAAG AGCAGAGAAG	1560
15	GAGCGAATCA TGAATGAGGA AGATCCTGAG AAACACGCCA GGCTGGAGGA GGCTGCATTG	1620
	AGGCCTGAGC AAAAGAAGTT GGAAAAGAAG CAAATGAAAA TGAAACAAAT CAAAGTGAAA	1680
	GCCCCATGTAA AGCCATCCCAGAGATTGAG TTCTGATGCC ACCTGTAAGC TCTGAATTCA	1740
20	CAGGAAACAT GAAAAACGCC AGTCCATTTC TCAACCTTAA ATTTCAGACA GTCTGGGCA	1800
	ACTGAGAAAT CCTTATTTCATC TCATCTACTC TGTTGGGT TTGGGTTTA CAGAGATTGA	1860
25	AGATACCTGG AAAGGGCTCT GTTTCCAAGA ATTTTTTTT CCAGATAATC AAATTATTTT	1920
	GATTATTITA TAAAAGGAAT GATCTATGAA ATCTGTGTAG GTTTAAATA TTTTAAAAT	1980
30	TATAATACAA ATCATCAGTG CTTTTAGTAC TTCAGTGTAA AAAGAAATAC CGTGAATTT	2040
	ATAGGTAGAT AACCAGATTG TTGCTTTTG TTTAAACCAA GCAGTTGAAA TGGCTATAAA	2100
	GACTGACTCT AAACCAAGAT TCTGCAAATA ATGATTGAA TTGACAATA AACATTGCTT	2160
35	GATGTTTCT ATTCAGGGA CCCAGAACAT AATGTAGTGT ATGTTTTAG GTGGGAGATG	2220
	CTGATAACAA ATTAATAGG AAGTCTGTAG GCATTAGGAT ACTGACATGT ACATGGAAA	2280
	TTCTAGGGAC AGGAGCATCA TTTTTCCCTT ACCTGATACC ACGAACAGT GACAACGTGA	2340
40	ATGCTGTATT TTAAGTGGTT GTAIGTTAT TTTCTGGAGT AACAAATGCA TGAAAATTA	2400
	ATGCTTCACC TAGGTAAGAT CATTGGTCTG TGTGAAATCA CAAATGTTT TTCTTCTTG	2460
45	GTGCTGCAG CCTGGTGGAT GTTCATGGAG AAGCTCTGTT CTCTATATTA TGGCTGTGTG	2520
	CCGTTGCTTC TCCCTCTGCT TTTATCTTTT CCACAGTTGA GGCTGGGTAT GTCTTTCAA	2580
	AGAAATGGCC ATGAATATGT GTAAGTATAC TTTTGAAAAT GAGCTTCCCT AACTATTGA	2640
50	GAGTTCTTTC CACCTCTTGC GGAACCAACT CTTGGAGGAG AGGCCATGT ATCTGCACGA	2700
	GCACCTAGCT TGTTCAAGATC TCTGCATTTT ATAAATGCTT CTTACCAAGA AAGCATTTTT	2760
55	AGGTCAATTGC TTGTACCAAGG TAATTTTGC CGGGATGGG TAAGGGTTGG GTTTCTGGT	2820
	GGGAGTGGGG TGGTGGGTAT TTTTGTGA TGCTTAGTG CAGGCCTGTT CTGAGGCAAT	2880
60	AACAAAGTTGC TGTGAAAACG CATGTGCTGC TGCCCTTGTA ACTGCCATGG AAACTTTCA	2940

135

	CATGGGTTTT TCTCCAAGTT AATACAGAAA TATGTAACT GAGAGATGCA AATGTAATAT	3000
	TTTTAACAGT TCATGAAGTT GTTATTAAAAA TAACTACAT AAAACTTAAT TACTTTAATA	3060
5	TTATATAATT ATAGTAGTGG CCTTGTTTA CAAACCTITA AATTACATTT TAGAAATCAA	3120
	AGTTGATAGT CTTAGTTATC TTTTGAGTAA GAAAAGCTTT CCTAAAGTC CATACTTIG	3180
10	GACCATGGCA GCTAATTTG TAACTTAAGC ATTCAATGAA ACTACCTATG GACATCTATT	3240
	AAAGTGATTG ACAAAAAAA	3259

## 15 (2) INFORMATION FOR SEQ ID NO: 32:

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 454 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:	
25	GGCACGAGGT CTTGCTCGG AAGAGTTAC GAGGTTTCAC CCACCTCTTC ATTCTTGAAC	60
	ATGCTTTTC TCTGCTTATT ACCCTCCCTG TTTCTCCTG GGCTGCCAAC AACACATTAT	120
30	ATTACCTCCA TCTGCAACCA GAGCTGCTAC CACCACTGTG CCCGAGCCTG AATTTTCATA	180
	GTTATATTAA AAAAATCAA GGTGCTGGGA TTACAGGCCT GAGCCACCGC GCCCGGCTGT	240
	AGCCCTGTC TTTATTCCCTC CCCGTCTAA CCCGTCTCA GCATGAATGC CAGAGTTACC	300
35	TCTTAAAWTA TGTCAGGGTG CTAGGCACAG TGGCTCATGC CTGTAATCCC AGCTCTTGGG	360
	AAGGCAGAGG CAGGAGGACA AMTTGACCC AGGAGTTGA GACCTGCTTG GGGAAATGTAG	420
40	TGAGACCTTG TTCTCCACAA AAAGGAAAAA AAAA	454

## (2) INFORMATION FOR SEQ ID NO: 33:

45	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 230 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:	
	GCTGCTATGG CTGAACCTTT ATTGANCGTG TTGTCTGTGC AGAGCGCTGT GCACGAGGTG	60
55	GAAGCAAACG AGGGAGGAAA ACAAAAGCCAC ACCCCTGCC ACAGAGGATG GAACAGAAGG	120
	CCCGCTGAGG TCAGGAAGGC AAGGTTGCCA CTAGGTGTTA CTGTGGGCC CAGATGCCGC	180
60	CATGCTGPTC ACCCTCAAA GGGTGGCATC TCAGCCCANG CAGTCCTCCT	230

## (2) INFORMATION FOR SEQ ID NO: 34:

## 5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

GGCACGAGGA AAGGCTGGCC TCTCTTCAAC ATGGGATCTT CTGGACTTTT GAGCCTCCTG	60
15 GTGCTATTTCG TCCCTCTTACG GAATGTCCAG GGACCTGGTC TGACTGATTG GTTATTCCCC	120
AGGAGATGTC CAAAATTCAG AGAAGAATGT GAATTCCAAG AAAGGGATGT GTGTACAAAG	180
20 GACAGACAAT GCCAGGACAA CAAGAAGTGT TGTGTCTTCA GCTGCGAAA AAAATGTTTA	240
GATCTCAAAC AAGATGTATG CGAAATGCCA AAAGAAACTG GCCCTGCCT GGCTTATTTT	300
CTTCATTGGT GGTATGACAA GAAAGATAAT ACTTGCTCCA TGTTGTCTA TGGTGGCTGC	360
25 CAGGGAAACA ATAACAACTT CCAATCCAAA GCCAACTGCC TGAACACCTG CAAGAATAAA	420
CGCTTTCCCT GATTGGATAA GGATGCCTG GAAGAACTGC CAGAATGTGG CTCATGCTCT	480
30 GAGTACTGTT CCTGTACCTG ACTGATGCTC CAGACTGGCT TCCAGTTTCA CTCTCAGCAT	540
TCCAAGATCT TAGCCCTTCC CAGAACAGAA CGCTTGATC TACCTCCTCT TCCTCCATCT	600
TTGGCTCTT TGATGCACAA TATCCATCCG TTTTGATTTTC ATCTTTATGT CCCCTTTATC	660
35 TCCAACCTCT AGAACTCCCA GTTTTACCT GTGTCACTCT CAATTTTTC CAGTAAAGTA	720
CTTGATGTAG TAAAAAAA AAAAAAAA AAA	753

40 (2) INFORMATION FOR SEQ ID NO: 35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1022 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CGCTCCTGCC GCCGGGACCC TCGACCTCCT CAGAGCAGCC GGCTGCCGCC CCCGGAAAGAT	60
GGCGAGGAGG AGCCGCCACC GCCTCCCT GCTGCTGCTG CGCTACCTGG TGGTCGCCCT	120
55 GGGCTATCAT AAGGCCTATG GGTTTCTGC CCCAAAGAC CAACAAGTAG TCACAGCAGT	180
AGWGTACCAA GAGGCTATTT TAGCCTGCAA AACCCCAAAG AAGACTGTTT SCTCCAGATT	240
60 AGAGTGGAAAG AAACCTGGTC GGAGTGTCTC CTTTGTCTAC TATCAACAGA CTCTTCAAGG	300

	TGATTTAAA AATCGAGCTG AGATGATAGA TTTCAATATC CGGATCAAAA ATGTGACAAG	360
	AA GTGATGCG GGGAAATATC GTTGTGAAGT TAGTCCCCA TCTGAGCAAG GCCAAAACCT	420
5	GGAAGAGGAT ACAGTCACTC TGGAAGTATT AGTGGCTCCA GCAGTTCCAT CATGTGAAGT	480
	ACCCCTTCT GCTCTGAGTG GAACTGTGGT AGAGCTACGA TGTCAAGACA AAGAAGGGAA	540
10	TCCAGCTCCT GAATACACAT GGTTAACAGA TGGCATCCGT TTGCTAGAAA ATCCCAGACT	600
	TGGCTCCAA AGCACCAACA GCTCATACAC AATGAATACA AAAACTGGAA CTCTGCAATT	660
	TAATACTGTT TCCAAACTGG ACACTGGAGA ATATTCCTGT GAAGCCCGCA ATTCTGTTGG	720
15	ATATCGCAGG TGTCTCTGGG AACGAATGCA AGTAGATGAT CTCAACATAA GTGGCATT	780
	AGCAGCCGTA GTAGTTGTGG CCTTAGTGTAT TTCCGTTGTGG TATGCTATGC	840
20	TCAGAGGAA GGCTACTTTT CAAAAGAAC CTCCCTCCAG AAGAGTAATT CTTCATCTAA	900
	AGCCACGACA ATGAGTGAAA ATGATTTCAA GCACACAAAA TCCTTATAA TTTAAAGACT	960
	CCACTTTAGA GATACACCAA AGCCACCGTT GTTACACAAG TTATTAAC ATTATAAAAC	1020
25	TC	1022

## (2) INFORMATION FOR SEQ ID NO: 36:

30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 3044 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
35	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:	
40	CTCTAAGAAC CTAGTGGATC CCCCGGCCCT GCAGGAATTC GGGCACGAGG GGAGACTGCT	60
	GTGGCTAAGG AGGGCGGGAA GGGCCCTCTG TGGGGCTGCC ATTTTGGCTG GGACCTAAAT	120
	GCAGTAAAGG ACCAGCTACG GGAATATAGA GAGTGGGCT TCCAGGCAGA GAAGCCTGCA	180
45	GTGCAAAGGT CTGCAGACAA CGACCTGGGC GTCTTCAAGG GACACAGGA ATCATATTGC	240
	CAGAACACAT TGTACAGGTA GCCAGGTGTC GGTCTCCAGC CTGAGAACTC TGGCTGTTGT	300
50	TCTTGTGTC GTCCCATATT CCTGCTGGC CTGGATGGA CATCAGCAAG GGCTCCAG	360
	GCATGCAGGG AGGCCTCCAC ATATGGATCT CTGAGAACCG GAAGATGGTG CCGGTACCCG	420
	AGGGGGCTTA CGGGAACTTT TTCGAGGAAC ACTGCTATGT CATCCTCCAC GTCCCCCAGA	480
55	GCCCCGAAGGY CACGCAGGGG GCGTCCAGCG ACCTGCCACTA CTGGGTGGG AAGCAGGCCG	540
	GTGCGGAAGC GCAGGGCGCT GCGGAGGCCT TCCAGCAGCG CCTACAGGAC GAGCTGGGG	600
60	GCCAGACCGT GCTGCACCGC GAGGCGCAGG GCCACGAGTC CGACTGCTTC TGCAGCTACT	660

	TCCGGCCCGGG AATCATCTAC AGGAAGGGAG GCCTAGCATC TGACCTCAAG CATGTGGAGA	720
	CCAAATTGTT CAACATCCAG CGACTGCTGC ACATCAAAGG GAGGAAGGCAC GTGCTGCCA	780
5	CTGAGGTGGA GCTCTCCTGG AACAGCTTTA ATAAGGGTGA CATCTTCCTG CTGGACCTAG	840
	GCAAGATGAT GATTCACTGG AATGGGCCAA AGACCACAT TTCTGAGAAG GCTCGGGGC	900
10	TGGVCTTGAC CTACAGCCTC CGGGACAGGG AACGTGGTGG TGGCTGTGCA CAGATTGGTG	960
	TGGTGGATGA TGAGGCCAA GCCCCGGACC TCATGAGAT CATGGAGGCT GTGCTGGGC	1020
	GCAGGGTGGG CAGMCTGCGT GCCGCCACGC CCAGCAAGGA TATCAACCAG CTGCAGAAGG	1080
15	CCAATGTTG CCTGTACCAT GTCTATGAGA AGGGCAAAGA CCTGGTGGTC CTGGAGTTGG	1140
	CGACCCCCCCC ACTGACCCAG GACCTGCTGC AGGAGGAGGA CTTCTACATC CTGGACCAGG	1200
20	GTGGCTCAA GATCTATGTG TGGCAGGGAC GCATGTCTAG CCTCCAGGAG AGAAAGGCTG	1260
	CCTTCAGCCG GGCTGTGGGC TTCATCCAGG CCAAGGGCTA CCCGACCTAC ACCAACGTGG	1320
	AGGTGGTGAA CGACGGGCCG GAGTCGGCCG CGTTCAAGCA GCTCTCCGG ACTTGGTCTG	1380
25	AGAACGGCG CAGGAACCAG AAGCTCGGCG GGAGGGATAA ATCGATTAT GTAAAGCTGG	1440
	ACGTGGGCAA GCTGCACACC CAGCCTAAGT TAGCGGCCA GCTCAGGATG GTGGACGACG	1500
30	GCTCTGGAA GGTGGAGGTG TGGTGCATCC AGGACTTACA CAGGCAGCCC GTGGACCCCA	1560
	AGCGTCATGG ACAGCTGTGT GCAGGCAACT GCTACCTTGT GCTCTACACCA TACCAGAGGC	1620
	TGGGCCGTGT CCAGTACATC CTGTACCTAT GGCAGGGCCA CCAGGCCACT GCGGATGAGA	1680
35	TTGAGGCCCT GAACAGCAAC GCTGAGGAAC TAGATGTCAT GTATGGTGGC GTCTTAGTAC	1740
	AGGAGCATGT GACCATGGGC AGCGAGCCCC CCCACTTCCT CGCCATCTTC CAGGGCCAGC	1800
40	TGGTGATCTT CCAGGAGAGA GCTGGGCACC ACGGAAAGGG GCAGTCAGCA TCCACCACAA	1860
	GGCTTTCCA AGTGCAAGGC ACTGACAGCC ACAACACCAAG GACCAGGGAG GTGCCAGCCC	1920
	GTGCCTCATC CCTCAACTCC AGTGACATCT TCTTGCTGGT CACAGCCAGC GTCTGCTACC	1980
45	TCTGGTTTGG GAAGGGCTGT AATGGTGATC AGCGTGAGAT GGCACGGGTG GTGGTCACTG	2040
	TCATTTCCAG GAAGAATGAG GAAACGGTGC TGGAGGGTCA GGAGCCTCCC CACTTCTGGG	2100
50	AGGCCCTGGG AGGCCGGGSC CCCTACCCCA GCAACAAGAG GCTCCCTGAG GAGGTCCCCA	2160
	GCTTCCAGGCC ACAGCTGTT GAGTGCTCCA CCCACATGGG CTGCCTGGTC CTGCGAGAAG	2220
	TGGGGTTCTT CAGCCAGGAG GACCTGGACA AGTATGACAT CATGTTACTG GACACCTGGC	2280
55	AGGAGATCTT CCTGTGGCTT GGGGAAGCTG CAAGTGAGTG GAAGGAGGCG GTGGCCTGGG	2340
	GCCAGGAGTA CCTGAAGACT CACCCAGCAG GGAGGAGCCC GGNACACACCC ATCGTGTGG	2400
60	TCAAGCAGGG CCATGAGCCT CCCACCTCA TTGGATGGTT CTTCACTTGG GACCCCTACA	2460

	AGTGGACTAG CCACCCATCC CACAAGGAAG TGGTGGATGG CAGCCGGCA GCAGCATCAA	2520
	CCATCTCTGA GATAACAGCA GAAGTCACA ACTTCCGGCT ATCCAGATGG CCGGGCAATG	2580
5	GCAGGGCAGG TGCGTGGCC CTGCAGGCC TCAAGGGCTC CCAGGACAGC TCAGAGAATG	2640
	ATCTGGTGGC AAGCCCCAAG TCGGCTGGCA GCAGAACAG CAGCTCGTC AGCAGCACCA	2700
10	GGGCCACGAT CAACGGGGC CTGCGCGGG AACAATGAT GCACCAGGCT GTTGAGGACC	2760
	TGCCAGAGGG CGTGGACCCCT GCCCCCAGGG AGTTCTATCT CTCAGACTCT GACTTCCAAG	2820
	ATATCTTGG GAAATCCAAG GAGGAATTCT ACAGCATGGC CACGTGGAGG CAGCGGCAGG	2880
15	AGAAAAAAGCA GCTGGCTTC TTCTGAACCC AAGCCCTCTC GACTGCCCCT ATCCCCTGGA	2940
	CCCCAACATA CCTACAATGC TGGGGAGGCC CTGCTTCCAC TCCCCTCAGA GGCTTTTGGT	3000
20	CATCCTCTGC GTGTCAGTAA AAGCAGGCAG CCCATAAAAA AAAA	3044

## (2) INFORMATION FOR SEQ ID NO: 37:

## 25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

	TTCAAGGATT ATAATATGCT GAGTAAACTT TTGGCACTAA GGAAGCCAGC TACAGGCCAC	60
35	GTAATGAAAA CTATTCAGAA AACAGTTCAAG CAAATACTAC TATTTGAATA CAGTTCAAAT	120
	CGTATTTATA TAAATACTCT GCCTACATTA TTTAACCAA ACTGGATTAT TCACCATTCT	180
40	TTGAAGATGC CTTGTGTTTT CTGTTATCTA CTTCTGCTCG TGCAAGTTAC TTACACCTTC	240
	ACCCCTTCAA ATCCTAACTTC TTCTTCAAGG CCTGATTCAG ATTAACTT TTTAAAGGCT	300
	ATCTGAATCA TTCAAGGGAG AAGATAACCT TTCTCTCATA AAAACACTTA GAGCAAAC TA	360
45	CCACTATTAA ATCACTTATT GCATACTGAA AAAAAAAAAA AAAAAAAACTC GAGGGGGGN	420
	CCGGTACCCA ATTGCCCCTA TAGTGAGTCG TATTACAATT CACTGGCCG TCGTTTTACA	480
50	ACGTCNTGAC TGGGAAAACC CTGGCGTTAC CCAACTTAAT CGCCTTGCA CACATCCCCC	540
	T	541

## 55 (2) INFORMATION FOR SEQ ID NO: 38:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

60

## (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

5	GTCGGCGGCG GCGGCGGCCG TTGAAGTAC TCGGAGCGAG GAGACCCGAG CGAGCAGACG	60
	CGGCCCTGGC GCCCGCCCTG CGCACTCAC C ATGGCGATGC ATTTCATCTT CTCAGATACA	120
10	CGGGTGCTTC TGTTTGATTT CTGGAGTGTC CACAGTCCTG CTGGCATGGC CCTTTGGTG	180
	TGGTGCTCC TGCTCTGGC TGACTGTAT GAAGGCATCA AGGTGGCAA AGCAAGCTGC	240
	TCAACCAGGT ACTGGTGAAC CTGCCAACCT CCATCAGCCA GCAGACCATC GCAGAGACAG	300
15	ACGGGACTC TGCAAGCTCA GATTCAATTCC CTGTTGGCAG AACCCACCAC AGGTGNTATT	360
	TGTGTCACCT TGCCAGTCT CTAATCCATG TCATCCAGGT GGTCATCGGC TACTTCATCA	420
20	TGCTGGCCGT AATGTCCTAC AACACCTGGA TTTTCCTTGG TGTTGCTTGT GGCTCTGCTG	480
	TGGGCTACTA CCTAGCTTAC CCACCTCTCA GCACAGCTTA GCTGGTGAGG AACGTGCAGG	540
	CACTGAGGCT GGAGGGACAT GGAGCCCCCT CTTCCAGACA CTATACTTCC AACTGCCCTT	600
25	TCTTCTGATG GCTATTCCCTC CACCTTATTCC CCAGCCCCTG GAAACTTGA GCTGAAGCCA	660
	GCACCTTGCTC CCTGGAGTTC GGAAGCCATT GCAGCAACCT TCCTCTCAG CCAGCCTACA	720
	TAGGGCCAG GCATGGCTT GTGCTTTAAG ACAGCTGCTG TGACCAAAGG GAGAATGGAG	780
30	ATAACAGGGG TGGCAGGGTT ACTGAGCCCA TGACAAATGCT TCTCTGTGAC TCAAACCAGG	840
	AATTTCAAA GATTTCAAGC CAGGGAGAAG GGTCTTGGT GATGCAGGGC ATGGAACCTG	900
35	GACACCCCTCA GCTCTCTGC TTTGTGCCCT ATCTACAGGA GCATGCCCA TTGGACTTCC	960
	TGACCTCTTC TGCTTTGAG GGACAGAGAC CAAGCTAGAT CCTTTTCTC ACCTTTCTGC	1020
40	CTTTGGAAACA CATGAAGATC ATCTCGCTA TGGATCATGT TGACAAACTA AGTTTTTTTT	1080
	ATTTTTCCCA TTGAACCTCCT AGTGGCAAT TTGACACATT CATAAAAAAA AATTTTTAAT	1140
	GAAATGATTT CATTGATTCA TGATGGATGG CAGAAACTGC TGAGACCTAT TTCCCTTTCT	1200
45	TGGGGAGAGA ATAAGTGACA GCTGATTAAGA GCCAGAGACA CAGGACTGCT TTCAGGGCTCC	1260
	TGGTTTATTTC TCTGATAGAC TGAGCTCCTT CCACCCAGAAG GCACTGCCTG CAGGAAGAAG	1320
50	AWGATCTGAT GCGCGTGGGT GTCTGGGAAG CTCTTCGTGG CCTCAATGCC CTCCCTTATC	1380
	CTCATCTTTC TTCTATGCAG AACAAAAAGC TGCATCTAAT AATGTTCAAT ACTTAATATT	1440
	CTCTATTTAT TACTTACTGC TTACTCGTAA TGATCTAGTG GGGAAACATG ATTCAATTAC	1500
55	TTAAAAATACT GATTAAGCCA TGGCAGGTAC TGACTGAAGA TGCAATCCAA CCAAAGCCAT	1560
	TACATTTTTT GAGTTAGATG GGACTSTCTG GATAGTGAA CCTCTTCACT TTATAAAAAA	1620
60	GGAAAGAGAG AAAATCACTG CTGTATACTA AATACCTCAC AGATTAGATG AAAAGATGGT	1680

	TGTAAGCTTT GGGATTAAA AACAAACAAA TACATTTAG TAAATATATA TTTTAAATA	1740
	AAAAAAAGAA AA	1752
5		
	(2) INFORMATION FOR SEQ ID NO: 39:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1907 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:	
	AGITCAAGGG CACAGGGCA CAGGCCACG ACTGCAGCG GATGGACCAG TACTGCATCC	60
20	TGGGCCGCAT CGGGGAGGGC GCCCAMGGCA TCGTCTTCAA GGCAAGCAC GTGGAGACTG	120
	GCGAGATAGT TGCCCTCAAG AAGGTGGCCC TAAGGCGTT GGAAGACGGC TTCCCTAAC	180
	AGGCCCTGCG GGAGATTAAG GCTCTGCAGG ARATGGAGGA CAATCAGTAT GTGGTACAAC	240
25	TGAAGGCTGT GTTCCCACAC GGTGGAGGCT TTGTGCTGGC CTTTGAGTTC ATGCTGTCGG	300
	ATCTGGCCGA GGTGGTGCAGC CATGCCAGA GGCCACTAGC CCAGGCACAG GTCAAGAGCT	360
30	ACCTGCAGAT GCTGCTCAAG GGTGTGCGCT TCTGCCATGC CAACAAACATT GTACATCGGG	420
	ACCTGAAACC TGCCAACCTG CTCATCAGCG CCTCAGGCCA GCTCAAGATA GCGGACTTTG	480
	GCCTGGCTCG AGTCTTTCTC CCAGACGGCA GCGCCTCTA CACACACCAG GTGGCCACCA	540
35	GGAGCTCACT GAGCTGCCGG ACTACAACAA GATCTCTTT AAGGAGCAGG TGCCCATGCC	600
	CCTGGAGGAG GTGCTGCCCTG ACGTCTCTCC CCAGGCATTG GATCTGCTGG GTCAATTCT	660
40	TCTCTACCCCT CCTCACCAGC GCATCGCAGC TTCCAAGGCT CTCCTCCATC AGTACTTCTT	720
	CACAGCTCCC CTGCCCTGCCA ATCCATCTGA GCTGCCGATT CCTCAGCGTC TAGGGGACC	780
	TGCCCCCAAG GCCCATCCAG GGCCCCCCC CATCCATGAC TTCCACGTGG ACCGGCCTCT	840
45	TGAGGAGTCG CTGTTGAACC CAGAGCTGAT TCGGCCCTTC ATCCTGGAGG GGTGAGAAGT	900
	TGGCCCTGGT CCCGTCTGCC TGCTCCTCAG GACCACTCAG TCCACCTGTT CCTCTGCCAC	960
50	CTGCCCTGGCT TCACCCCTCCA AGGCCCTCCCC ATGGCCACAG TGGGCCACA CCACACCCCTG	1020
	CCCCCTAGCC CTTGCGARGG TTGGTCTCGA GGCAGAGGTC ATGTTCCAG CCAAGAGTAT	1080
	GAGAACATCC AGTCGAGCAG AGGAGATTCA TGGCCTGTGC TCGGTGAGCC TTACCTTCTG	1140
55	TGTGCTACTG ACGTACCCAT CAGGACAGTG AGYTCCTGCTG CCAGTCAAGG CCTGCATATG	1200
	CAGAATGACG ATGCCTGCCCT TGGTGTGCT TCCCCGAGTG CTGCCCTCTG GTCAAGGAGA	1260
60	AGTGCAGAGA GTAAGGTGTC CTTATGTGAG AACTCAAGT GGAAGGAAGA TTTGGTTTGG	1320

	TTTTATTCTC AGAGCCATTA AACACTAGTT CAGTATGTGA GATATAGATT CTAAAAACCT	1380
	CAGGTGGCTC TGCCTTATGT CTGTTCTTC TTCATTCTC TCAAGGGAAA TGGCTAAGGT	1440
5	GGCATTGTCT CATGGCTCTC GTTTTGCCCC TCATGGGGAG GGTAGCACCA GGCGATAGCCA	1500
	CTTTTGCCCC GAGGGACTCC TGTTGTCTTC ACATCACTGA GCACATCATIT AGAACTGAGG	1560
10	GAGACAGAAG TCTAGGCCCA GGGATGGCTC CAGTTGGGA TCCAGCAGGA GACCCTCTGC	1620
	ACATGAGGCT GGTITACCAA CATCTACTCC CTCAGGATGA CGGTGAGCCA GAAGCAGCTG	1680
	TGTATTTAACG GAAACAAGCG TTCTTGGAAAT TAATTTATAA ATTTAATAAA TCCCAATATA	1740
15	ATCCCAGCTA GTGCTTTTTC CTTATTATAA TTTGATAAGG TGATTATAAA AGATACATGG	1800
	AAGGAAGTGG AACCAGATGC AGAAGAGGAA ATGATGGAAG GACTTATGGT ATCAGATACC	1860
20	AATATTTAAA AGTTTGTATA ATAATAAAGA GTATGATTGT GGTTCAA	1907

## (2) INFORMATION FOR SEQ ID NO: 40:

25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1114 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:	
	GGGCAGACGA TGCTGAAGAT GCTCTCCTTT AAGCTGCTGC TGCTGGCCGT GGCTCTGGGC	60
35	TTCTTTGAAG GAGATGCTAA GTTGGGGAA AGAAACGAAG GGAGCGGACA AGGAGGAGAA	120
	GGTGCCTGAA TGGGAACCCC CGGAAGCGCC TGAAAAGGAG AGACAGGAGG ATGATGTCCC	180
40	AGCTGGAGCT GCTGAGTGGG GGAGAGATGC TGTGCGGTGG CTTCTACCCCT CGGCTGTCCC	240
	GCTGCCCTCG GAGTGACAGC CGGGGGCTAG GGCGCTGGA GAATAAGATA TTTCCTGTTA	300
	CCAACAACAC AGAATGTGGG AAGTTACTGG AGGAAATCAA ATGTGCACTT TGCTCTCCAC	360
45	ATTCTCAAAG CCTGTTCCAC TCACCTGAGA GAGAAGCTTT GGAAAGAGAC CTAGTACTTC	420
	CTCTGCTCTG CAAAGACTAT TGCAAAGAAT TCTTTTACAC TTGCCGAGGC CATATTCCAG	480
	GTTTCCCTCA AACAACTGCG GATGAGTTTT GTTTTACTA TGCAAGAAAA GATGGTGGGT	540
50	TGTGCTTTCC AGATTTTCCA AGAAAACAAG TCAGAGGACC AGCATCTAAC TACTTGGACC	600
	AGATGGAAGA ATATGACAAA GTGGAAGAGA TCAGCAGAAA GCACAAACAC AACTGCTTCT	660
55	GTATTCAAGA GGTGTGAGT GGGCTGCGC AGCCCGTTGG TGCCCTGCAT AGTGGGGATG	720
	GCTCGCAACG TCTCTTCATT CTGGAAAAAG AAGGTTATGT GAAGATACTT ACCCCTGAAG	780
60	GAGAAATTTT CAAGGAGCCT TATTTGGACA TTCACAAACT TGTCAAAAGT GGAATAAAGG	840

	TGGGCTTTT AAATTTTATT TATTTTGTCG CTGGCTACGT TAATTTTATT TTAGTGTAC	900
	CTTCCTCACT GAAGGTATT CTTTGTATAA AAAGAAAGAA TCTTCAGGA GAAAATAAGG	960
5	GGGCAACATA AGAAACAATA ATTATGGCAC CTGAATTAGG ACAGTGACAT TAAAKGTTGG	1020
	CTKTTTAWAT TTTAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA	1080
10	AAAAAAA AAAAAAAA AAAAAAAA AAAA	1114

## (2) INFORMATION FOR SEQ ID NO: 41:

15           (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1652 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

	TTGGCACCTC TAATTGCTCT CGTGTATTG GTGCCCGAC TTTCACGATG GCTCGCCCAA	60
25	CCTTACTACC TTCTGTGGC CCTGCTCTCT GCTGCCITCC TACTCGTGAG GAAACTGCCG	120
	CCGCTCTGCC ACGGTCTGCC CACCCAACGC GAAGACGGTA ACCCGTGTGA CTTTGACTGG	180
30	AGAGAAGTGG AGATCCTGAT GTTTCTCAGT GCCATTGTGA TGATGAAGAA CCCCAGATCC	240
	ATCACTGTGG AGCAACATAT AGGCAACATT TTCAATGTTA GTAAAGTGGC CAACACAATT	300
	CTTTTCTTCC GCTTGGATAT TCGCATGGGC CTACTTTACA TCACACTCTG CATACTGTTTC	360
35	CTGATGACGT GCAAACCCCC CCTATATATG GGSCCTGAGT ATATCAAGTA CTTCAATGAT	420
	AAAACCATTG ATGAGGAAC AGAACGGGAC AAGAGGGTCA CTTGGATTGT GGAGTTCTTT	480
	GCCAATTGGT CTAATGACTG CCAATCATTT GCCCCTATCT ATGCTGACCT CTCCCTTAAA	540
40	TACAACGTGA CAGGGCTAAA TTTTGGGAAG GTGGATGTG GACGCTATAC TGATGTAGT	600
	ACGCGGTACA AAGTGAGCAC ATCACCCCTC ACCAAGCAAC TCCCTACCT GATCCTGTT	660
45	CAAGGTGGCA AGGAGGCAAT GCGGGGGCCA CAGATTGACA AGAAAGGACG GGCTGTCTCA	720
	TGGACCTTCT CTGAGGAGAA TGTGATCCGA GAATTAACT TAAATGAGCT ATACCAGCGG	780
	GCCAAGAAC TATCAAAGGC TGGAGACAAT ATCCCTGAGG ACCAGCCTGT GGCTTCAACC	840
50	CCCACCACAG TGTCAGATGG GGAAAACAAG AAGGATAAAAT AAGATCCTCA CTTGGCAGT	900
	GCTTCTCTC CTGTCAATTG CAGGCTCTTT CCATAACCAC AAGCCTGAGG CTGCAGCYTT	960
55	TTATTTATGT TTTCCTTGT GCTGTGACTG GGTGGGGCAG CATGCAGCTT CTGATTTAA	1020
	AGAGGCATCT AGGGAATTGT CAGGCACCC ACAGGAAGGC CTGCCATGCT GTGGCCAAGT	1080
60	GTTCACCTGG AGCAAGAAAG AGATCTCATA GGACGGAGGG GGAAATGGTT TCCCTCCAAG	1140

	CTTGGGTYAG TGTGTTAACT GCTTATCAGC TATTCAGACA TCTCCATGGT TTCTCCATGA	1200
	AACTCTGTGG TTTCATCATT CCTTCTTAGT TGACCTGCAC AGCTGGTTA GACCTAGATT	1260
5	TAACCCCTAAG GTAAGATGCT GGGGTATAGA ACGCTAAGAA TTTTCCCCCA AGGACTCTTG	1320
	CTTCCTTAAG CCCTTCTGGC TTCGTTATG GTCTTCATTA AAACTATAAG CCTAACCTTG	1380
10	TCGCTAGTCC TAAGGAGAAA CCTTTAACCA CAAAGTTTT ATCATTGAAG ACAATATTGA	1440
	ACAACCCCCCT ATTTCGTGGG GATTGAGAAG GGCTGANTAG AGGCCTTGAGA CTTCCTTTG	1500
	TGTGGTAGGA CTTGGAGGAG AAATCCCCTG GACTTCACT AACCCCTCTGA CATACTCCCC	1560
15	ACACCCAGTT GATGGCTTTC CGTAATAAAA AGATTGGAT TTCCCTTTGA AAAAAAAAAAA	1620
	AAAAAGGGGG CCGCTCTAGN GGTNCCANGC TT	1652

20

(2) INFORMATION FOR SEQ ID NO: 42:

	(i) SEQUENCE CHARACTERISTICS:	
25	(A) LENGTH: 1473 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:	
30	GGCACGGAGCC GCGGGGCTGT CACCTCCGCC TCTGCTCCCC GACCCGGCCA TGCGCGGCCT	60
	CGGGCTCTGG CTGCTGGCG CGATGATGCT GCCTGCGATT GCCCCCAGCC GGCCTGGC	120
35	CCTCATGGAG CAGTATGAGG TCGTGTGTCG GTGGCGTCTG CCAGGCCCCC GAGTCCGCC	180
	AGCTCTGCCCT TCCCACITGG GCCTGCACCC AGAGAGGGTG AGCTACGTCC TTGGGGCCAC	240
40	AGGGCACAAC TTCACCCCTCC ACCTGCGGAA GAACAGGGAC CTGCTGGCT CCGGCTACAC	300
	AGAGACCTAT ACGGCTGCCA ATGGCTCCGA GGTGACGGAG CAGCCTCGCG GGCAGGGACCA	360
	CTGCTTCTAC CAGGGCCACT TAGAGGGTAC CGGACTCAGC CGCCAGCCTC AGCACCTGTG	420
45	CCGGCCTCAG GGGTTTCTTC CAGGTGGGGT CAGACCTGCA CCTGATCGAG CCCCTGGATG	480
	AAGGTGGCGA GGGCGGACGG CACGCCGTGT ACCAGGCTGA GCACCTGCTG CAGACGGCCG	540
50	GGACCTGCGG CGTCAGCGAC GACAGCCTGG GCAGCCTCCT GGGACCCCCGG ACGGCAGCCG	600
	TCTTCAGGCC TCGGCCCCGGG GACTCTCTGC CATCCCGAGA GACCCGCTAC GTGGAGCTGT	660
	ATGTGGTCGT GGACAATGCA GAGTTCCAGA TGCTGGGGAG CGAACGAGCC GTGCGTCATC	720
55	GGGTGCTGGA CGTGGTGAAT CACGTGGACA AGCTATATCA GAAACTCAAC TTCCGTGTGG	780
	TCCTGGTGGG CCTGGAGATT TGGAATAGTC AGGACAGGTT CCACGTCAGC CCCGACCCCCA	840
60	GTGTCACACT GGAGAACCTC CTGACCTGGC AGGCACGGCA ACGGACACGG CGGCACCTGC	900

	ATGACAACGT ACAGCTCATC ACGGGTGTG ACTTCACCGG GACTACTGTG GGGTTTGCCA	960
	GGGTGTCCGC CATGTGCTCC CACAGCTCAG GGGCTGTGAA CCAGGACCAC AGCAAGAAC	1020
5	CCGTGGGCCT GGCCCTGCACC ATGGCCCATG AGATGGGCCA CAACCTGGGC ATGGACCATG	1080
	ATGAGAACGT CCAGGGCTGC CGCTGCCAGG AAACGGCTTCG AGCCCGGGCG CTGCATCATG	1140
10	GCAAGGCCAG CATTGGCTCC CAGTTTCCCC AGGATGTTCA GTGACTGCAG CCAGGCCTAC	1200
	CTGGAGAGCT TTTTGGAGCG GCCGCAGTCG GTGTGCCCTCG CCAACGCCCG TGACCTCAGC	1260
	CACCTGGTGG GGGGCCCCGT GTGTGGGAAC CTGTTTGTGG AGCGTGGGGA GCAGTGGCAC	1320
15	TGCGGGCCCCC CCGAGGACTG CCGGAACCGC TGCTGCAACT CTACCCACCTG CCAGCTGGCT	1380
	GAGGGGGCCC AGTGTGCGCA CGGTACCTGC TGCCAGGAGT GCAAGGTGAA GCCGGCTGGT	1440
20	GAGCTGTGCC GTCCCAAGAA GGACATGTGT GAC	1473

## (2) INFORMATION FOR SEQ ID NO: 43:

25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 772 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:	
	TCGGTTCTC TCTTTGCAGG AGCACCGGCA GCACCACTGT GTGAGGGGAG CAGGCAGCGG	60
35	TCCTAGCCAG TTCCCTGATC CTGCCAGACC ACCCAGCCCC TGGCACAGAG CTGCTCCACA	120
	GGCACCATGA GGATCATGCT GCTATTACA GCCATCTGG CCTTCAGCCT AGCTCAGAGC	180
40	TTCGGGGCTG TCTGTAAGGA GCCACAGGAG GAGGTGGTTC CTGGCGGGGG CCCGAGCAAG	240
	AGGGATCCAG ATCTCTACCA GCTGCTCCAG AGACTCTTCA AAAGCCACTC ATCTCTGGAG	300
	GGATTGCTCA AAGCCCTGAG CCAGGYTAGC ACAGATCCTA AGGAATCAAC ATCTCCCGAG	360
45	AAACGTGACA TGCTGACTTT CTGGTGGGA YTTATGGCA AGAGGAGCGT CCAGCCAGAC	420
	TCTCCTACGG ATGTGAATCA AGAGAACGTC CCCAGCTTG GCATCCTCAA GTATCCCCCG	480
	AGAGCAGAAT AGGTACTCCA CTTCCGGACT CCTGGACTGC ATTAGGAAGA CCTCTTTCCC	540
50	TGTCCCAATC CCCAGGTGCG CACGCTCCTG TTACCCCTTC TCTTCCCTGT TCTTGTAAACA	600
	TTCTTGTGCT TTGACTCCTT CTCCATCTTT TCTACCTGAC CCTGGTGTGG AACTGCTATA	660
55	GTGAATATCC CCAACCCCAA TGGGCATTGA CTGTAGAATA CCCTAGAGTT CCTGTAGTGT	720
	CCTACATTA AAATATAATG TCTCTCTCTA TTCCTCAACA AATAAAGGAT TT	772

## (2) INFORMATION FOR SEQ ID NO: 44:

## (i) SEQUENCE CHARACTERISTICS:

- 5                   (A) LENGTH: 403 base pairs  
                  (B) TYPE: nucleic acid  
                  (C) STRANDEDNESS: double  
                  (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

10	AATTTCGGCAC GAGCNGTGGAA TGGGAGGCTA CGGAAGAGAT GGAATGGATA ATCAGGGAGG	60
	CTATGGWTCA KTTGGAAGAW TGGGAATGGG GAACAATTAC AGTGGAGGT ATGGTACTCC	120
15	TGATGGTTTG GGTGGTTATG GCCGTGGTGG TGGAGGCAGT GGAGGTTACT ATGGGCAAGG	180
	CGGCATGAGT GGAGGTGGAT GGC GTGGGAT GTACTGAAAG CAAAAACACC AACATACAAG	240
20	TCTTGACAAC AGCATCTGGT CTACTAGACT TTCTTACAGA TTTAATTCTC TTTGTATTTC	300
	AAGAACTTTA TAATGACTGAGGAAATGTGT TTTCAAAATA TTATTTGGTA AAGAACAGA	360
	TTGTGATGGG GAAAAAAA AAAAAAAGAA TTCAAAAGC TTC	403

25

## (2) INFORMATION FOR SEQ ID NO: 45:

## (i) SEQUENCE CHARACTERISTICS:

- 30                   (A) LENGTH: 928 base pairs  
                  (B) TYPE: nucleic acid  
                  (C) STRANDEDNESS: double  
                  (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

35	CCTCTCGCTA ATTAACCAA TTGCCAAA GGGGATGTT CCCTGCAANG CCAATTAAAT	60
40	TTGGGTAAAC CCCCAGGNTT TTCCCCAAGT CCACGACGTT GTAAAAAACG ACAGCCCAAT	120
	TGAAATTGTW AAAAACSAAC YCACTAANAG GGCAAATGG GTNACSGGGC CCCCCCCCAGA	180
	RTTTTTTTTT TTGTTTTTTCT CTGRTTGWCA ATGAGRATAT TTATTGAGGG TTTATTGAGT	240
45	GCAGGGAGAA GGGCTKGATG MCTTGGGRTG GGAGGAGAGA CCCCTCCCT GGGATCCTGC	300
	AGCTCYAGKC TCCCGTGGGT GGGGGTKAGR GTTGRGAACC TATGAACATT CTGTAGGGGC	360
50	CACTGTCCTTC TCCACGGTGC TCCCTTCATG CGTGACCTGG CAGCTGTAGC TTCTGTGGGA	420
	CTTCCACTGC TCRGGCGTCA GGTCAGGTA GCTGCTGCC GCGTACTTGT TGGTGTCTYTG	480
	TTTGGAGGGT KTGGTGGTCT CCACTCCCGC CTTGACGGGG CTGCYATCTG CNTTCCAGGC	540
55	CACTGTCACR GCTCCCGGGT AGAAGTCACT KATSAGACAC ACYAGTGTGG CCTTGTGGC	600
	TTGRAGCTCC TCAGAGGAGG CGGGGAACAG AGTGACMGWG GGGKYRGCC TGGGCTGACC	660
60	TAGGACGGTG ACCTTGGTCC CAGTTCCGAA GACMCCATGA TTACCACTGC TGTCTGTGA	720

	GTAACAGTAG TAGTCAGCCG CATCCTCCAC CTGGGCCCA CTGATAGTCA AGGTGGCAC	780
	TGTCCCTGAR CTGGAGCCAR AGAATCTCTS AGGGATCCGG AGGGTCGTTT GTTGTCTCA	840
5	TAGATGACCA GGCACAGGGG CCTGGCCTGA CTTCTGKTGG TACCAATAWA CATATTTCTT	900
	CGGCAATGCA TCTCCAGGAG CAGGTGAT	928
10	(2) INFORMATION FOR SEQ ID NO: 46:	
	(i) SEQUENCE CHARACTERISTICS:	
15	(A) LENGTH: 885 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:	
	GGCACGGAGGG AATCTGCACC ATGCCCTGGG TTCTGCTCCT CCTGACCCCTC CTCACTCACT	60
	CTGCAGTGTC AGTGGTCCAG GCAGGGCTGA CTCAGCCCCC CTCGGTGTCC AAGGACTTGA	120
25	GACAGACCGC CACACTCACC TGCAACGGGA ACAACAACAA TGTTGGCGAC CAAGGAGCAG	180
	CTTGGCTGCA GCAGCACCAG GGCCACCCCTC CCAAACCTCT GTCCTACAGG AATAATAACC	240
30	GGCCCTCAGG GATCTCAGAG AGATTATCTG CATCCAGGTC AGGAGCCACA TCCTCCCTGA	300
	CCATTACTGG ACTCCAGCCT GAGGACGAGG CTGACTATTA CTGCGCAGCA TATGACAGCA	360
	GCCTCGCAGT TTGGATGTTC GGCGGAGGGA CCAAGCTGAC CGTCCTAGGT CAGCCAAGG	420
35	CTGCCCCCTC GGTCACTCTG TTCCCACCT CCTCTGAGGA GCTTCAAGCC AACAGGCCA	480
	CACTGGTGTG TCTCATAAAGT GACTTCTACC CGGGAGCCGT GACAGTGGCC TGGAAGGCAG	540
40	ATAGCAGCCC CGTCAAGGCG GGAGTGGAGA CCACCAACACC CTCCAAACAA AGCAACAACA	600
	AGTACGGGGC CAGCAGCTAC CTGAGCCTGA CGCTCTGAGCA GTGGAAGTCC CACAAAAGCT	660
	ACAGCTGCCA GGTCACGCAT GAAGGGAGCA CCGTGGAGAA GACAGTGGCC CCTACAGAAT	720
45	GTTCATAGGT TCTCATCCCT CACCCCCAC CACGGGAGAC TAGAGCTGCA GGATCCCAGG	780
	GGAGGGGTCT CTCCCTCCAC CCCAAGGCAT CAAGCCCTTC TCCCTGCACT CAATAAACCC	840
50	TCAATAATAA TTCTCATTGT CAATCAGAAA AAAAAAAA AAAA	885

	(2) INFORMATION FOR SEQ ID NO: 47:	
55	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 2315 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
60		

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

	TTTTTTTTT TTTGATTTT CAAAATTAAC TTTTTTATTA ATTTAAAAAT CCAGAAAATAC	60
5	AGTGACTACA TAAATAAGTA CCATAATTAG GTACATGTCC TGTGAGAAC A GTGAAAGGGT	120
	AATACTGTTA TGTTACTCTT ACTTGTTAAC ATGAGTTAAC TAGAAAATGG CTACAACTGC	180
10	TAAATGATGC TTATGGTC TT TGTTGTTCCA AGTGTATG ATACAAATAA ATACACAAGA	240
	AGAACACACAT CCATTCTTCT CTACTAACTA CAGGCAGCTT GGCCCTTTA CCCTATGTCC	300
	TATTCTCTAC ACAACACCAA ACACTGGAGG GTTCTACTT TGACTTAACA CAGCTCCCCA	360
15	GCTCCCTGCTT CCCACAGCAT TTGCAAAAGG TGTGTCCAG CACCTGGAGG CAGGAGTATA	420
	TCTAGGGAAA CTCTCTGCGT GTTCTCTTAA GGCTAAGCTT TCAGAGAAC A CCTGGGTGGG	480
20	AAGGCTTTGG GATGAATCAT CCAGAAGGAG AAACACCTCT TTGCTTCTAGG ATCTAGTTAC	540
	TAGTCTCCAC ATTATGGAAT CACTGCCACC TCTGGACGG AGGGAGCAGC CGCATAACAC	600
	CTTCCCCCTT TTACACACACA CACACACACA CACACACAAA GGAGCAAATT	660
25	ATGCTGTGCA TGGCGTGAAT AATTGACTGC ATTTGAGTTT GGAGTTTCTAGG GGCACTGTG	720
	ACTTAAGCAA AATAAGCCTG CAGTCCAGCT GCAGCTTGAG TTTTCTTGCT TTACCTATC	780
30	CAAAACTGTC TGTCTTGCT AACAGTGGCC CTTTCAGAT CTCTCCAGGT ACAAAACCTT	840
	GACTAAATCT TCAAGCTCTG TTCTGCATAC ACAGACTGAA CACATCTGGC TGATCTGAGC	900
	TTCTCCCTCG GTGAAGATCT TCCACTGGCT CAGGGTGTGTT CTGGTCACCA GCTTGAAGTG	960
35	AGGAAGCTCC TCAAACATCC TCTTGGAGAT CTTCTCAATA TGGAAGTGCT GGAGAATGCC	1020
	CTTTCGAATA GTCCAAACGT GGACCTCTAC CTGAGGTGGT CTCTCAGTCT CCAGTGCTAT	1080
40	TTTTCTGGTT GTCTCCCCAT CCTCCATGAA TACAGACTCA TACACAGGCA TCGTTCTTC	1140
	CCCGCAGAAG TAGCCTTAT TGTCAAAGCT TTGGCTGGA AGTTCTCTG GACACACCTT	1200
	GCAGCACTTT CCGCTCTATT TTTGAGGATA CTTGCAGGGG TATCGATTGG GGCACTGGAT	1260
45	TTTCTTACAC TCTTGGCTGG TGACATTACA AGTACATAGC ACACACTCCA CAATGCCAAA	1320
	TGCCCCGGAGG TTTGGGTGCC AGGACTCGCC ATGAGAACAG GTCTTCCAT TGAAACACA	1380
50	CACCTGTCCA TGCTTGTGTT TGTTATTGAT GACAATTGCA ACAATGGTTC CTGATGCTTG	1440
	CTGGGAATCC ATAAGAGCTC CCCGGTGAAT TCTGGCCCCA GGAAAGCGGG ACAGACCTCC	1500
	AGCCTGTCCG CTTGGTGGAG GATCATAGTG AGAGCGGTGG TAAGAACGTC TTGCTTCTCT	1560
55	GTTGGCAGGT TGCCGGAAGA TATCACCACATC AGAATGTTCC CATGACAGTT CTCCATCTCC	1620
	TCTGCATACC CGGCAGCAGG AATCTGGAAC AGAGACTGGG AAGGCACAGG TTAATTGGG	1680
60	CCAAGTCTTG AGACCACAAAT ACACGTTCC CTCCGAACAG CTGCACTGGG TGCATTGATT	1740

	GGGTTGCCGA TTCTGAAAGA GCCCTTCAGC TACGAACAGC TCTCCATGTT GGTAAGTTGT	1800
	CCCCATTGTAC TCGCAAGACT TGCTGGTCAC CTTATTGTT ACTGGGGGTA AGGAGTCTTC	1860
5	TGGGCAGCGA GGGCAGCACA GATGAGGAAT ATGCACAGGA GAAAGGCAAT GAACATTTGG	1920
	ACATCTGACT CGGCTGCAA GCACATTCCC ATTCTCTGAG CAGATGCAGT TCACGCAGTA	1980
10	AACCAACCCA TAAGGTTCCA GGTAAGGATG CCATCTCTCA CCCACTCTGT ACTTCTTGTC	2040
	TTGAAAACATG CAATAATGTCT CTGAATGTTT TACTTGTCT GTTGTGCCCTC CTTCCTAGCAA	2100
	AAGAAAAGCTC GTGCCGAATT CCTGCAGCCC GGGGGGATCC ACTAGTTCTA GAGCGGCCGC	2160
15	CACCGCGGTG GGAGCTCCAG CTTTTGGTTTC CCTTTAGTGA GGGGTTAATT TCGAGCTTGG	2220
	CGGTAATCAT GGGTCATAGC TTGTTTCTG GTGTTGAAAT TGGNTATCCC GCTCACAAAT	2280
20	TCCACAACAA CAATACGAGC CGGAAGCATA ANGTN	2315

## (2) INFORMATION FOR SEQ ID NO: 48:

25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 3175 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:	
	TTTTTTTGT CAATCACTTT AATAGATGTC CATAGGTAGT TCATATGAAT GCTTAAGTTA	60
35	CAAAATTAGC TGCCATGGTC CAAATGTATG GGACTTTAGG AAACCTTTTC TTACTCAAAA	120
	GATAACTAAG ACTATCAACT TTGATTCTA AAATGTAATT TAAAGTTTG TAAAACAAGG	180
40	CCACTACTAT AATTATATAA TATTAAGTA ATTAAGTTTT ATGTTAGTTA TTTTAATAAC	240
	AACTTCATGA ACTGTTAAAA ATATTACATT TGCATCTCTC AGTTACATA TTTCITGTATT	300
	AACTTGGAGA AAAACCCATG TGAAAAGTTT CCATGCAGTT ACAAAGGCAG CAGCACATGC	360
45	TGTTTTCACA GCAACTTGTG ATTGCTCAG AACAGGCCTG CACTAAAGCA TCAACAAAAA	420
	ATACCCACCA CCCCACCTCC ACCAGAAAAC CCAACCCCTA CCCATCCCCG GCAAAAATTA	480
	CCTGGTACAA GCAATGACCTT AAAATGCTT TCTTGGTAAG AAGCATTAT AAAATGCAGA	540
50	GATCTGAACA AGCTAAGTGC TCGTGCAGAT ACATGGGCCT CTCCTCCAAG AGTTGGTTCC	600
	GCAAGAGGTG GAAAGAACTC TCAATAGTTT AGGAAAGCTC ATTTCAAAA GTATACTTAC	660
55	ACATATTCACT GCCCAATTCT TTGAAAGAAC ATACCCAGCC TCAACTGTGG AAAAGATAAA	720
	AGCAGAGGGGA GAAGCAACGG CACACAGCCA TAATATAGAG AACAGAGCTT CTCCATGAAC	780
60	ATCCACCAGG CTGCAGCAAC CAAGAAGGAA AAAACATTG TGATTCACA CAGACCAATG	840

150

	ATCTTACCTA GGTGAAGCAT TAAATTTTCA TGCATTGTT ACTCAAGAAA ATAAACATAC	900
	AACCACTTAA AATAACAGCAT TCACGTTGTC ACTGGTTCGT GGTAATCAGGT AAGGAAAAAA	960
5	TGATGCTCCT GTCCCTAGAA TTTTCCATGT ACATGTCAGT ATCCTAACGC CTACAGACTT	1020
	CCTATTAATT TTGTTATCAG CATCTCCCAC CTAAAACAT ACACATACATT ATGTTCTGGG	1080
10	TCCCTGAAAT AGAAAACATC AAGCAATGTT TATTGTGCAA TTCCAATCAT TATTTCAGA	1140
	ATCTTGGTT AGAGTCAGTC TTTATAGCCA TTTCAACTGC TTGGTTAAA CAAAAAGCAA	1200
	CAATCTGGTT ATCTTACCTAT AAATTCAYG GTATTTCTTT AAACACTGAA GTACTAAAAG	1260
15	CACTGATGAT TTGTATTATA ATTTTTAAAA TTTTAAAAC CTACACAGAT TTCTAGATTC	1320
	ATTCCCTTTA TAAAATAATC AAAATAATTG GATTATCTGG AAAAAAAAT TCTTGAAACA	1380
	GAGCCCTTTC CAGGTATCTT CAATCTCTGT AAAACCCAA ACCCAAACAA GAGTAGATGA	1440
20	TGAAATAAGG ATTTCTCAGT TGCCCAAGAC TGTCTGAAAT TTAAGGTTGA GAAATGGACT	1500
	GGCGTTTTTC ATGTTTCTG TGAATTCAAGA GCTTACAGGT GGCACTCAGAA CTCAAATCTC	1560
25	TGGGATGGCT TTACATGGCT TTCACCTTGA TTTGTTCAT TTTCATTTGC TTCTTTCCA	1620
	ACTTCTTTTK CTCACGCCCT AATGCAGCCT CCTCCAGCCT GCGCTGTTTC TCAGGATCTT	1680
30	CCTCATTCTAT GATTGCTCC TTCTCTGCTC TTTTTTCTC CTCCCCCGGA GACTGTGCTG	1740
	CTTCCTGTCT TTGCACATGT GTCAGTTCA AGAAGTTCTC TTCTACTCGG GCACGGTTCT	1800
	TATCTGCTTT TTGTTTGCCT TCTCTGTGA GTCGGAACCT TTTGGCTTTA TCAATAGAAT	1860
35	AAATCACCAT GTTCATCAGG GGTAGCAGTG CCTCCATATC CTTTGGTAA GTGTTACCTG	1920
	AGCCAGGCAC ATTAAATGTA AACAAACAGTG TCCCTTTAGT GTCAGGTAGC TTTAAAGGCT	1980
	GACCTTCCTC TTGCATAATT TTTGGACCAAG AGAAACTGGTC TGAAAATGA ACAGATTCAA	2040
40	TCTTGTCAAG ATAGTGTGTA AGAAAGTGAA CCATCTTTGT ATCCATCATT CGCTCTGTGA	2100
	CTTCTCCCAT CTCTGACAGG ATGGCCAAAG AGTCCGGCAG TCCATACTTT GCTCCAGACT	2160
45	TAGGTTTATC ACTACAAAAC TCACTCAAAT CCTGCATCTC TTTCTGTAGT CGCACCAAGG	2220
	CTTTCCGTGT CCCAACAGCA AATACGTAGG TATCCATGTC TTCATCATTC ATGGTTACCTT	2280
	TTATTTGCAC TTGATCACTC ACTGGCCTCA TCATCCGGC CAGGACATTG AGTAAGTCTT	2340
50	GTCTCTTGAG GAACCTCAGC TGGATAAGCA TGCCCTCACA GCACACTCGA CCAGAACACC	2400
	ACAGGTTATA GATGTGCTCA TTCTCCTGGT TCAACTTTCC TGTGTTGTG GCTTCTTTGT	2460
55	TAGTTCCATC ATCCCCCACT AAAGTAAAGT TGCTCTCAA AAGCTCCCTA TGAGTGTAA	2520
	ACCAAGGCCTG TGCAAGGCGA CTGTTTTAT TCTTCCCAAT GATGTAATTG ATGATATAAG	2580
60	CAAGCAGACC AGTCACCATC AAAATTCATA GATAATAACT CTCCCAGCTG TTCTGGAGGT	2640

	GTGCAGGAAC ATCAACAATC GTTATTGGGT CTTTATTTTT GCTAGAAGAA GTATCTGGTT	2700
	TGTCCTCATA ACCTTCAAAT TCTTCATCAT CATATGGTTC ACTCTCAGTA TCTCCCTCCT	2760
5	GGGTATCTGC ATCTTCAAAA TCTCCPTCTT GGTTTCATC CTGCCCTCC AACTCCACAG	2820
	TGGCTCATC TTCATCATCT TCAGTGATTA TGACCCGTTG AGGAGATTCA GTAACAGAGT	2880
10	CTTCCATGAC ATCCTCAAAT TCAGCGAAGT CATTATCATC ATACTCTACT ATGTCCTCCT	2940
	CATCCTCAAAT ATCATCAAAC TTGGCTTCAG AGACACTCCC AAACACCAGA AGGACAACAC	3000
	AGAAAAGTGTG GAAGGCTTTC ATTGCACCTT GAGAAAAAAA GCTGTGGCCG AAGCCGAAAC	3060
15	CCGGCCCGAGC GCCCTGCGTC CGACACCCCT GCCCCGGCTG CTCTCGGCCT GGCGCCGCC	3120
	TCCCGCGATCG CAGCGGTTTT ACTGCCCGG ATGCCTCTAG GACGCAGCCA GAACC	3175

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(2) INFORMATION FOR SEQ ID NO: 49:

	(i) SEQUENCE CHARACTERISTICS:	
25	(A) LENGTH: 783 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:	
30	GGCACCGCGGA AAGGCTGGCC TCTCTTCAMC ATGGGMCCTT CTGGACTTTT GAGCCTCCTG	60
	GTGCTATTCTG TCCTCTTAGC GAATGTCCAG GGACCTGGTC TGACTGATTG GTTATTTCCC	120
35	AGGAGATGTC CCAAAATCAG AGAAGAATGT GAATTCCAAG AAAGGGATGT GTGTACAAAG	180
	GACAGACAAT GCCAGGACAA CAAGAAGTGT TGTGTCTTCA GCTGCGAAA AAAATGTTTA	240
40	GATCTAAAC AAGATGTATG CGAAATGCCA AAAGAAACTG GCCCCCTGCCCT GGCTTAITTT	300
	CTTCATTGGT GGTATGACAA GAAAGATAAT ACTTGCTCCA TGTTTGTCTA TGGTGGCTGC	360
	CAGGGGAAAC AATAACAAC TCCAATCCAA AGCCAACACTGC CTGAACACCT GCAAGAATAA	420
45	ACGCTTTCCC TGATTGGATA AGGATGCACT GGAAGAACTG CCAGAATGTG GCTCATGCTC	480
	TGAGTACTGT TCCTGTACCT GACTGTGCT CCAGACTGGC TTCCAGTTTC ACTCTCAGCA	540
	TTCCAAGATC TTAGCCCTTC CCAGAACAGA ACGCTTGATC CTACCTCCCTC TTCCCTCCATC	600
50	TTTGGCTTT TTGATGCACA ATATCCATCC GTTTTGATTT CATCTTTATG TCCCCTTTAT	660
	CTCCAACCTTC TAGAACTCCC AGTTTATACC TGTGTCACTC TCAATTTTTT CCAGTAAAGT	720
55	ACTTGATGTW GAAAAAAAAA AAAAAAAA AAAACGGCA CGAGGGGGG CCCGGTACCC	780
	AAT	783

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## (2) INFORMATION FOR SEQ ID NO: 50:

## (i) SEQUENCE CHARACTERISTICS:

- 5                   (A) LENGTH: 3030 base pairs  
                  (B) TYPE: nucleic acid  
                  (C) STRANDEDNESS: double  
                  (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

10	CTCTAAGAAC CTAGTGGATC CCCCCGGCCT GCAGGAATTC GGGCACGGAG GGGAGACTTN	60
	CTGTGGCTAA GGGAGGGCGG GAAGGGCCCT CTGTGGGCT GCCATTTGGG CTGGGACCTA	120
15	AATGCAGTAA AGGAGCAGCT ACGGGAATAT AGAGAGTGAG GCTTCCAGGC AGAGAACGCT	180
	GCAGTGCAAA GGCTCTGCAGA CAACGACCTG GGCGTCTTCA AGGGACACAA GGAATCATAT	240
20	TGCCAGAAC AATTGTACAG GTAGGCCAGGT GTCGGTCTCC AGCCTGAGAA CTCTGGCTGT	300
	TGTTCCCTTGT GTCGTCCCCT ATTCCCTGCCT GGCTGCGAT GGACATCAGC AAGGGCCTCC	360
	CAGGCATGCA GGGAGGCCTC CACATATGGA TCTCTGAGAA CCGGAAGATG GTGCCGGTAC	420
25	CCGAGGGGGC TTACGGGAAC TTTTCGAGG AACACTGCTA TGTCATCCTC CACGTCCCC	480
	AGAGCCCGAA GGYCACGCAG GGGCGTCCA GCGACCTGCA CTACTGGTC GGGAAAGCAGG	540
30	CGGGTGCGGA AGGCAGGGC GCTGCGGAGG CCTTCCAGCA GCGCCTACAG GACGAGCTGG	600
	GGGGCCAGAC CGTGTGCAC CGCGAGGCAGC AGGGCCACGA GTCCGACTGC TTCTGCAGCT	660
	ACTTCCGCCG GGGAAATCATC TACAGGAAGG GAGGCCTAGC ATCTGACCTC AAGCATGTGG	720
35	AGACCAAATT GTTCAACATC CAGCGACTGC TGCACATCAA AGGGAGGAAG CACGTGTCTG	780
	CCACTGAGGT GGAGCTCTCC TGGAACAGCT TTAATAAGGG TGACATCTTC CTGCTGGACC	840
40	TAGGCAAGAT GATGATTCAAG TGGAAATGGC CCAAGACCAG CATTCTGAG AAGGCTCGGG	900
	GGCTGGYCTT GACCTACAGC CTCCGGGACA GGGAACGTGG TGGTGGCTGT GCACAGATIG	960
	GTGTGGTGGG TGATGAGGCC AAAGCCCCGG ACCTCATGCA GATCATGGAG GCTGTGCTGG	1020
45	GCCGCAGGGT GGGCAGMCTG CGTGYCCCA CGCCCGACAA GGATATCAAC CACGTGCAGA	1080
	AGGCCAATGT TCGCCTGTAC CATGTCTATG AGAAGGGCAA AGACCTGGTG GTCCCTGGAGT	1140
50	TGGCGACCCC CCCACTGACC CAGGACCTGC TGCAAGGAGGA GGACTTCTPAC ATCCCTGGACC	1200
	AGGGTGGCTT CAAGATCTAT GTGTGGCAGG GACCGATGTC TAGCCTCCAG GAGAGAAAGG	1260
	CTGCCCTTCAG CCGGGCTGTG GGCTTCATCC AGGCAAGGG CTACCCGACC TACACCAACG	1320
55	TGGAGGTGGT GAACGACGGC GCGGAGTCGG CCGCGTTCAA GCAGCTCTTC CGGACTTGGT	1380
	CTGAGAAGCG GCGCAGGAAC CAGAAGMTCG GCGGGAGGGA TAAATCGATT CATGTAAAGC	1440
60	TGGACGTGGG CAAGCTGCAC ACCCAGCCTA AGTTAGCGGC CCAGCTCAGG ATGGTGGACG	1500

	ACGGCTCTGG GAAGGTGGAG GTGTGGTGC A TCCAGGACTT ACACAGGCAG CCCGTGGACC	1560
	CCAAGCGTCA TGGACAGCTG TGTGCAGGCA ACTGCTACCT TGTGCTCTAC ACATACCAGA	1620
5	GGCTGGGCCG TGTCCAGTAC ATCCTGTACC TATGGCAGGG CCACCAGGCC ACTGCGGATG	1680
	AGAATTGAGGC CCTGAACAGC AACGCTGAGG AACTAGATGT CATGTATGGT GGCCTCCCTAG	1740
10	TACAGGAGCA TGTGACCATG GGCACCGAGC CCCCCCACTT CCTCGCCATC TTCCAGGGCC	1800
	AGCTGGTGAT CTTCAGGAG AGACGCTGGC ACCACGGAAA GGGGCAGTCA GCATCCACCA	1860
	CAAGGCTTTT CCAAGTGCAA GGCACGTACA GCCACAAACAC CAGGACCATG GAGGTGCCAG	1920
15	CCCCGTGCC TC ATCCCTCAAC TCCAGTACA TCTTCTTGCT GGTCACAGCC AGCGTCTGCT	1980
	ACCTCTGGTT TGGGAAAGGG CTGTAATGGT GATCAGCGTG AGATGGCACG GGTGGTGGTC	2040
20	ACTGTCAATT CCAGGAAGAA TGAGGAAACG GTGCTGGAGG GTCAGGAGCC TCCCCACTTC	2100
	TGGGAGGCC CGGGAGGCC GGGCCCCCTA CCCCAGCAAC AAGAGGCTCC CTGAGGAGGT	2160
	CCCCAGCTTC CAGCCACGAC TGTTTGAGTG CTCCAGCCAC ATGGCTGCC TGGTCCCTCGC	2220
25	AGAAGTGGGG TTCTTCAGCC AGGAGGACCT GGACAAGTAT GACATCATGT TACTGGACAC	2280
	CTGGCAGGAG ATCTTCCTGT GGCTTGGGGA AGCTGCAAGT GAGTGGAAAGG AGGCAGGTGGC	2340
30	CTGGGGCCAG GAGTACCTGA AGACTCACCC AGCAGGGAGG AGCCCGNCA CACCCATCGT	2400
	GCTGGTCAAG CAGGGSCATG AGCCTCCCAC CTTCATTTGA TGGTTCTTCA CTTGGGACCC	2460
	CTACAAGTGG ACTAGGCCACC CATCCCACAA GGAAGTGGTG GATGGCAGCC CGGCAGCAGC	2520
35	ATCAACCATC TCTGAGATAA CAGCAGAACT CAACAACTTC CGGCTATCCA GATGGCCGGG	2580
	CAATGGCAGG GCAGGTGCCG TGGCCCTGCA GGCCTCAAG GGCTCCAGG ACAGCTCAGA	2640
40	GAATGATYTG GTGCGAAGCC CCAAGTCGGC TGGCAGCAGA ACCAGCAGCT CCGTCAGCAG	2700
	CACCAACGCC ACCATCAACG GGGGCTGCG CGGGGAACAA CTGATGCACC AGGCTGTTGA	2760
	GGACCTGCCA GAGGGCGTGG ACCCTGCCCG CAGGGAGTTC TATCTCTCAG ACTCTGACTT	2820
45	CCAAGATATC TTGGGAATT CCAAGGAGGA ATTCTACAGC ATGCCACGT GGAGGCAGCG	2880
	GCAGGAGAAA AAGCAGCTGG GCTTCTCTG AACCCAAGCC CTCTCGACTG CCCCTATCCC	2940
50	CTGGACCCCA ACATACCTAC AATGCTGGG AGGCCCTGCT TCCACTCCCC TCAGAGGCTT	3000
	TTGGTCATCC TCTGCGTGTC AGTAAAAGCA	3030

## 55 (2) INFORMATION FOR SEQ ID NO: 51:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

	Met	Glu	His	Ala	Ala	Gly	Leu	Pro	Val	Thr	Arg	His	Pro	Leu	Ala	Leu
5	1				5				10					15		
	Leu	Leu	Ala	Leu	Cys	Pro	Gly	Pro	Phe	Pro	Ala	Leu	Leu	Leu	Pro	Leu
		20				25				30						
10	Leu	Pro	Trp	Gly	Tyr	Pro	Leu	Ala	Pro	Pro	Gly	Leu	Cys	Lys	Leu	Pro
		35				40				45						
	Gln	Gly	Ala	Pro	Leu	Pro	Cys	Ser	Ser	Xaa	Leu	Thr	Ser			
		50				55				60						

15

## (2) INFORMATION FOR SEQ ID NO: 52:

	(i) SEQUENCE CHARACTERISTICS:															
20	(A) LENGTH:	243	amino acids													
	(B) TYPE:	amino acid														
	(D) TOPOLOGY:	linear														
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:															
25	Met	Asp	Gln	Tyr	Cys	Ile	Leu	Gly	Arg	Ile	Gly	Glu	Gly	Ala	Xaa	Gly
	1					5			10			15				
	Ile	Val	Phe	Lys	Ala	Lys	His	Val	Glu	Thr	Gly	Glu	Ile	Val	Ala	Leu
30				20			25			30						
	Lys	Lys	Val	Ala	Leu	Arg	Arg	Leu	Glu	Asp	Gly	Phe	Pro	Asn	Gln	Ala
		35				40				45						
35	Leu	Arg	Glu	Ile	Lys	Ala	Leu	Gln	Glu	Met	Glu	Asp	Asn	Gln	Tyr	Val
		50				55			60							
	Val	Gln	Leu	Lys	Ala	Val	Phe	Pro	His	Gly	Gly	Gly	Phe	Val	Leu	Ala
		65				70			75				80			
40	Phe	Glu	Phe	Met	Leu	Ser	Asp	Leu	Ala	Glu	Val	Val	Arg	His	Ala	Gln
		85				90				95						
	Arg	Pro	Leu	Ala	Gln	Ala	Gln	Val	Lys	Ser	Tyr	Leu	Gln	Met	Leu	Leu
45			100			105			110							
	Lys	Gly	Val	Ala	Phe	Cys	His	Ala	Asn	Asn	Ile	Val	His	Arg	Asp	Leu
		115				120			125							
50	Lys	Pro	Ala	Asn	Leu	Leu	Ile	Ser	Ala	Ser	Gly	Gln	Leu	Lys	Ile	Ala
		130				135			140							
	Asp	Phe	Gly	Leu	Ala	Arg	Val	Phe	Ser	Pro	Asp	Gly	Ser	Arg	Leu	Tyr
		145				150			155			160				
55	Thr	His	Gln	Val	Ala	Thr	Arg	Ser	Ser	Leu	Ser	Cys	Arg	Thr	Thr	Thr
		165				170			175							
	Arg	Ser	Pro	Leu	Arg	Ser	Arg	Cys	Pro	Cys	Pro	Trp	Arg	Xaa	Cys	Cys
		180				185			190							
60																

155

Leu Thr Ser Leu Pro Arg His Trp Ile Cys Trp Val Asn Ser Phe Ser  
195 200 205

5 Thr Leu Leu Thr Ser Ala Ser Gln Leu Pro Arg Leu Ser Ser Ile Ser  
210 215 220

Thr Ser Ser Gln Leu Pro Cys Leu Pro Ile His Leu Ser Cys Arg Phe  
225 230 235 240

10 Leu Ser Val

15 (2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Met Glu Ala Lys Phe Gly Leu Leu Cys Phe Leu Val Ser Thr Pro Trp  
1 5 10 15

25 Ala Glu Leu Leu Ser Leu Leu His Leu Thr Gln Val Pro Phe Pro  
20 25 30

Gly Ser Gln Gly Pro Gly Phe  
35

30

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

40 Met Leu Ala Arg Lys Ala Glu Arg Gly Ser Met Gly Thr Ala Arg Asp  
1 5 10 15

Ser His Ile Leu Leu Val Cys Ser Val Val His Pro Ala Ser Ala Gln  
20 25 30

45 Pro Val Tyr Thr Val  
35

50 (2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

Met Leu Ser Phe Lys Leu Leu Leu Ala Val Ala Leu Gly Phe Phe  
1 5 10 15

60

Glu Gly Asp Ala Lys Phe Gly Glu Arg Asn Glu Gly Ser Gly Ala Arg  
 20 25 30

5 Arg Arg Arg Cys Leu Asn Gly Asn Pro Pro Lys Arg Leu Lys Arg Arg  
 35 40 45

Asp Arg Arg Met Met Ser Gln Leu Glu Leu Leu Ser Gly Gly Glu Met  
 50 55 60

10 Leu Cys Gly Gly Phe Tyr Pro Arg Leu Ser Cys Cys Leu Arg Ser Asp  
 65 70 75 80

Ser Pro Gly Leu Gly Arg Leu Glu Asn Lys Ile Phe Ser Val Thr Asn  
 85 90 95

15 Asn Thr Glu Cys Gly Lys Leu Leu Glu Glu Ile Lys Cys Ala Leu Cys  
 100 105 110

20 Ser Pro His Ser Gln Ser Leu Phe His Ser Pro Glu Arg Glu Val Leu  
 115 120 125

Glu Arg Asp Leu Val Leu Pro Leu Leu Cys Lys Asp Tyr Cys Lys Glu  
 130 135 140

25 Phe Phe Tyr Thr Cys Arg Gly His Ile Pro Gly Phe Leu Gln Thr Thr  
 145 150 155 160

Ala Asp Glu Phe Cys Phe Tyr Tyr Ala Arg Lys Asp Gly Gly Leu Cys  
 165 170 175

30 Phe Pro Asp Phe Pro Arg Lys Gln Val Arg Gly Pro Ala Ser Asn Tyr  
 180 185 190

35 Leu Asp Gln Met Glu Glu Tyr Asp Lys Val Glu Glu Ile Ser Arg Lys  
 195 200 205

His Lys His Asn Cys Phe Cys Ile Gln Glu Val Val Ser Gly Leu Arg  
 210 215 220

40 Gln Pro Val Gly Ala Leu His Ser Gly Asp Gly Ser Gln Arg Leu Phe  
 225 230 235 240

Ile Leu Glu Lys Glu Gly Tyr Val Lys Ile Leu Thr Pro Glu Gly Glu  
 245 250 255

45 Ile Phe Lys Glu Pro Tyr Leu Asp Ile His Lys Leu Val Gln Ser Gly  
 260 265 270

Ile Lys Val Gly Phe Leu Asn Phe Ile Tyr Phe Cys Ala Gly Tyr Val  
 50 275 280 285

Asn Phe Ile Leu Val Leu Pro Ser Ser Leu Lys Val Phe Leu Cys Asn  
 290 295 300

55 Lys Arg Lys Asn Leu Ala Gly Glu Asn Lys Gly Ala Thr  
 305 310 315

60 (2) INFORMATION FOR SEQ ID NO: 56:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Met Ser Trp Gly Ile Trp Lys Gly Leu Asp Leu Phe Pro Leu Ile Lys  
1 5 10 15

10 Gly Asn Ser Ser Leu Cys Leu Phe Leu Leu Val Val Pro Lys Gly Tyr  
20 25 30

15 Ser Ser Ser Glu Ile Thr Arg Ala Leu  
35 40

## 20 (2) INFORMATION FOR SEQ ID NO: 57:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

Met Ser Leu Pro Cys His Leu Leu Pro Gly Leu Leu Gln Gln Leu Leu  
1 5 10 15

30 Thr Ser Leu Pro Ala Phe Gln Phe Ser Ala Pro Leu Gln Val Phe Ser  
20 25 30

Leu Asp Gly Leu Ser Leu Pro Ala Pro Lys Leu Leu Thr Ala Ser Leu  
35 40 45

35 Cys Leu Gln Asp Glu Val Arg Ala Val  
50 55

40

## (2) INFORMATION FOR SEQ ID NO: 58:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

50 Asn Leu Ile Phe Phe Ser Ile Thr Ile Tyr Ser Tyr Lys Lys Gly Ala  
1 5 10 15

Ser Glu Lys Gly His Cys Arg Leu Cys Pro Leu Ala Ser Phe Val Ile  
20 25 30

55

## (2) INFORMATION FOR SEQ ID NO: 59:

## (i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 296 amino acids

(B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

5	Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg				
	1	5	10	15	
	Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu				
	20	25	30		
10	Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly				
	35	40	45		
15	Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg				
	50	55	60		
	Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn				
	65	70	75	80	
20	Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe				
	85	90	95		
	Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met				
	100	105	110		
25	Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys				
	115	120	125		
30	Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys				
	130	135	140		
	Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val				
	145	150	155	160	
35	Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile				
	165	170	175		
	Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly				
	180	185	190		
40	Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val				
	195	200	205		
45	Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln				
	210	215	220		
	Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg				
	225	230	235	240	
50	Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn				
	245	250	255		
	Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp				
	260	265	270		
55	Asn Ile Pro Glu Glu Gln Pro Val Xaa Ser Thr Pro Thr Thr Val Ser				
	275	280	285		
60	Asp Gly Glu Asn Lys Lys Asp Lys				
	290	295			

## (2) INFORMATION FOR SEQ ID NO: 60:

5

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

Met Arg Ala Phe Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val Pro Met  
1 5 10 15

15 Leu Leu Leu Ile Val Gly Gly Ser Phe Gly Leu Arg Glu Phe Ser Gln  
20 25 30

Ile Arg Tyr Asp Ala Val Lys Ser Lys Met Asp Pro Glu Leu Glu Lys  
35 40 45

20 Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu Ser Glu Tyr Glu Lys Ile  
50 55 60

25 Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn Ile Arg Gly Pro Arg Pro  
65 70 75 80

Trp Glu Asp Pro Asp Leu Leu Gln Gly Arg Asn Pro Glu Ser Leu Lys  
85 90 95

30 Thr Lys Thr Thr  
100

## 35 (2) INFORMATION FOR SEQ ID NO: 61:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

Met Ile Gln Leu Ile Leu Gln Phe Trp Tyr Leu Phe Ser Met Leu Leu  
1 5 10 15

45 Lys Pro Val Gln Gln Cys Gln His Cys Ser Gln Ile Thr Pro Ser Gly  
20 25 30

50 Thr Met Pro Thr Ser Glu Thr Val Phe Leu Ile Leu Phe Leu Pro  
35 40 45

## 55 (2) INFORMATION FOR SEQ ID NO: 62:

60

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

Met Ser Ala Pro Ala Pro Ser Cys Ser Ala Ser Gly Ile  
1 5 10

5

(2) INFORMATION FOR SEQ ID NO: 63:

10                   (i) SEQUENCE CHARACTERISTICS:  
                      (A) LENGTH: 335 amino acids  
                      (B) TYPE: amino acid  
                      (D) TOPOLOGY: linear  
                      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

15 Met Arg Gly Leu Gly Leu Trp Leu Leu Gly Ala Met Met Leu Pro Ala  
1 5 10 15

Ile Ala Pro Ser Arg Pro Trp Ala Leu Met Glu Gln Tyr Glu Val Val  
 20 25 30

20 Leu Pro Xaa Arg Leu Pro Gly Pro Arg Val Arg Arg Ala Leu Pro Ser  
35 40 45

25 His Leu Gly Leu His Pro Glu Arg Val Ser Tyr Val Leu Gly Ala Thr  
50 55 60

Gly His Asn Phe Thr Leu His Leu Arg Lys Asn Arg Asp Leu Leu Gly  
65 70 75 80

30 Ser Gly Tyr Thr Glu Thr Tyr Thr Ala Ala Asn Gly Ser Glu Val Thr  
85 90 95

Glu Gln Pro Arg Gly Gln Asp His Cys Phe Tyr Gln Gly His Val Glu  
 100 105 110

Gly Tyr Pro Asp Ser Ala Ala Ser Leu Ser Thr Cys Ala Gly Leu Arg  
115 120 125

40 130 135 140

145 150 155 160

165 170 175

Leu Leu Gly Pro Arg Thr Ala Ala Val Phe Arg Pro Arg Pro Gly Asp  
180 185 190

Ser Leu Pro Ser Arg Glu Thr Arg Tyr Val Glu Leu Tyr Val Val Val  
195 200 205

55 Asp Ash Ala Glu Phe Gin Met Leu Gly Ser Glu Ala Ala Val Arg His  
           210                   215                   220

Arg Val Leu Glu Val Val Ash His Val Asp Lys Leu Tyr Gin Lys Leu	225	230	235	240
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00 Asn Phe Arg Val Val Leu Val Gly Leu Glu Ile Trp Asn Ser Gln Asp

60 Asn Phe Arg Val Val Leu Val Gly Leu Glu Ile Trp Asn Ser Gln Asp

	245	250	255
	Arg Phe His Val Ser Pro Asp Pro Ser Val Thr Leu Glu Asn Leu Leu		
	260	265	270
5	Thr Trp Gln Ala Arg Gln Arg Thr Arg Arg His Leu His Asp Asn Val		
	275	280	285
	Gln Leu Ile Thr Gly Val Asp Phe Xaa Gly Thr Thr Val Gly Phe Ala		
10	290	295	300
	Arg Val Ser Thr Met Cys Ser His Ser Ser Gly Ala Val Asn Gln Asp		
	305	310	315
	His Ser Lys Asn Pro Val Gly Val Ala Cys Thr Met Ala His Glu		
15	325	330	335

## 20 (2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

	Met	Pro	Gln	Lys	Lys	Arg	Phe	Leu	Met	Leu	Phe	Gly	Leu	Leu	Met	Ala
	1			5				10						15		
30	Cys Leu															

## 35 (2) INFORMATION FOR SEQ ID NO: 65:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 125 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

	Met	Leu	Ser	Gln	Pro	Leu	Val	Gly	Ala	Gln	Arg	Arg	Arg	Ala	Val	
	45	1			5			10			15					
	Gly Leu Ala Val Val Thr Leu Leu Asn Phe Leu Val Cys Phe Gly Pro															
					20		25		30							
50	Tyr Asn Val Ser His Leu Val Gly Tyr His Gln Arg Lys Ser Pro Trp															
					35		40		45							
	Trp Arg Ser Ile Ala Val Xaa Phe Ser Ser Leu Asn Ala Ser Leu Asp															
					50		55		60							
55	Pro Leu Leu Phe Tyr Phe Ser Ser Ser Val Val Arg Arg Ala Phe Gly															
					65		70		75		80					
60	Arg Gly Leu Gln Val Leu Arg Asn Gln Gly Ser Ser Leu Leu Gly Arg															
					85		90		95							

Arg Gly Lys Asp Thr Ala Glu Gly Thr Asn Glu Asp Arg Gly Val Gly  
 100 105 110

5 Gln Gly Glu Gly Met Pro Ser Ser Asp Phe Thr Thr Glu  
 115 120 125

10 (2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

Met Arg Leu Val Phe Phe Gly Val Ser Ile Ile Leu Val Leu Gly  
 1 5 10 15

20 Ser Thr Phe Val Ala Tyr Leu Pro Asp Tyr Arg Cys Thr Gly Cys Pro  
 20 25 30

25 Arg Ala Trp Asp Gly Met Lys Glu Trp Ser Arg Arg Glu Ala Glu Arg  
 35 40 45

Leu Val Lys Tyr Arg Glu Ala Asn Gly Leu Pro Ile Met Glu Ser Asn  
 50 55 60

30 Cys Phe Asp Pro Ser Lys Ile Gln Leu Pro Glu Asp Glu  
 65 70 75

35 (2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

Met Arg Ile Met Leu Leu Phe Thr Ala Ile Leu Ala Phe Ser Leu Ala  
 1 5 10 15

45 Gln Ser Phe Gly Ala Val Cys Lys Glu Pro Gln Glu Glu Val Val Pro  
 20 25 30

50 Gly Gly Gly Arg Ser Lys Arg Asp Pro Asp Leu Tyr Gln Leu Leu Gln  
 35 40 45

Arg Leu Phe Lys Ser His Ser Ser Leu Glu Gly Leu Leu Lys Ala Leu  
 50 55 60

55 Ser Gln Ala Ser Thr Asp Pro Lys Glu Ser Thr Ser Pro Glu Lys Arg  
 65 70 75 80

Asp Met His Asp Phe Phe Val Gly Leu Met Gly Lys Arg Ser Val Gln  
 85 90 95

60

Pro Asp Ser Pro Thr Asp Val Asn Gln Glu Asn Val Pro Ser Phe Gly  
 100 105 110

5 Ile Leu Lys Tyr Pro Pro Arg Ala Glu  
 115 120

10 (2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

Met Val Val Met Glu Val Leu Met Thr Met Val Ala Ile Ile Thr  
 1 5 10 15

20 Ala Met Gly Met Met Ala Leu Met Thr Glu  
 20 25

25 (2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

Met Pro Trp Val Leu Leu Leu Leu Thr Leu Leu Thr His Ser Ala Val  
 1 5 10 15

35 Ser Val Val Gln Ala Gly Leu Thr Gln Pro Pro Ser Val Ser Lys Asp  
 20 25 30

40 Leu Arg Gln Thr Ala Thr Leu Thr Cys Thr Gly Asn Asn Asn Asn Val  
 35 40 45

Gly Asp Gln Gly Ala Ala Trp Leu Gln Gln His Gln Gly His Pro Pro  
 50 55 60

45 Lys Leu Leu Ser Tyr Arg Asn Asn Asn Arg Pro Ser Gly Ile Ser Glu  
 65 70 75 80

Arg Leu Ser Ala Ser Arg Ser Gly Ala Thr Ser Ser Leu Thr Ile Thr  
 85 90 95

50 Gly Leu Gln Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Tyr Asp  
 100 105 110

55 Ser Ser Leu Ala Val Trp Met Phe Gly Gly Thr Lys Leu Thr Val  
 115 120 125

Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser  
 130 135 140

60 Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser

164

145	150	155	160
Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser			
	165	170	175
5	Pro Val Lys Ala Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn		
	180	185	190
Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp			
10	195	200	205
Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr			
	210	215	220
15	Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser		
	225	230	235

## 20 (2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

Met Asp Ser Gln Gln Ala Ser Gly Thr Ile Val Gln Ile Val Ile Asn			
1	5	10	15
Asn Lys His Lys His Gly Gln Val Cys Val Ser Asn Gly Lys Thr Tyr			
30	20	25	30
Ser His Gly Glu Ser Trp His Pro Asn Leu Arg Ala Phe Gly Ile Val			
35	35	40	45
Glu Cys Val Leu Cys Thr Cys Asn Val Thr Lys Gln Glu Cys Lys Lys			
	50	55	60
Ile His Cys Pro Asn Arg Tyr Pro Cys Lys Tyr Pro Gln Lys Ile Asp			
40	65	70	75
	80		
Gly Lys Cys Cys Lys Val Cys Pro Glu Glu Leu Pro Gly Gln Ser Phe			
	85	90	95
45	Asp Asn Lys Gly Tyr Phe Cys Gly Glu Glu Thr Met Pro Val Tyr Glu		
	100	105	110
Ser Val Phe Met Glu Asp Gly Glu Thr Thr Arg Lys Ile Ala Leu Glu			
50	115	120	125
Thr Glu Arg Pro Pro Gln Val Glu Val His Val Trp Thr Ile Arg Lys			
	130	135	140
55	Gly Ile Leu Gln His Phe His Ile Glu Lys Ile Ser Lys Arg Met Phe		
	145	150	155
	160		
Glu Glu Leu Pro His Phe Lys Leu Val Thr Arg Thr Thr Leu Ser Gln			
60	165	170	175

Trp Lys Ile Phe Thr Glu Gly Glu Ala Gln Ile Ser Gln Met Cys Ser  
 180                    185                    190

5      Ser Arg Val Cys Arg Thr Glu Leu Glu Asp Leu Val Lys Val Leu Tyr  
 195                    200                    205

Leu Glu Arg Ser Glu Lys Gly His Cys  
 210                    215

10

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:  
 15      (A) LENGTH: 492 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

20      Met Lys Ala Phe His Thr Phe Cys Val Val Leu Leu Val Phe Gly Ser  
 1                5                10                15

Val Ser Glu Ala Lys Phe Asp Asp Phe Glu Asp Glu Asp Ile Val  
 20                25                30

25      Glu Tyr Asp Asp Asn Asp Phe Ala Glu Phe Glu Asp Val Met Glu Asp  
 35                40                45

30      Ser Val Thr Glu Ser Pro Gln Arg Val Ile Ile Thr Glu Asp Asp Glu  
 50                55                60

Asp Glu Thr Thr Val Glu Leu Glu Gly Gln Asp Glu Asn Gln Glu Gly  
 65                70                75                80

35      Asp Phe Glu Asp Ala Asp Thr Gln Glu Gly Asp Thr Glu Ser Glu Pro  
 85                90                95

Tyr Asp Asp Glu Glu Phe Glu Gly Tyr Glu Asp Lys Pro Asp Thr Ser  
 100                105                110

40      Ser Ser Lys Asn Lys Asp Pro Ile Thr Ile Val Asp Val Pro Ala His  
 115                120                125

45      Leu Gln Asn Ser Trp Glu Ser Tyr Tyr Leu Glu Ile Leu Met Val Thr  
 130                135                140

Gly Leu Leu Ala Tyr Ile Met Asn Tyr Ile Ile Gly Lys Asn Lys Asn  
 145                150                155                160

50      Ser Arg Leu Ala Gln Ala Trp Phe Asn Thr His Arg Glu Leu Leu Glu  
 165                170                175

Ser Asn Phe Thr Leu Val Gly Asp Asp Gly Thr Asn Lys Glu Ala Thr  
 180                185                190

55      Ser Thr Gly Lys Leu Asn Gln Glu Asn Glu His Ile Tyr Asn Leu Trp  
 195                200                205

60      Cys Ser Gly Arg Val Cys Cys Glu Gly Met Leu Ile Gln Leu Arg Phe  
 210                215                220

Leu Lys Arg Gln Asp Leu Leu Asn Val Leu Ala Arg Met Met Arg Pro  
 225                    230                    235                    240  
 5   Val Ser Asp Gln Val Gln Ile Lys Val Thr Met Asn Asp Glu Asp Met  
 245                    250                    255  
 Asp Thr Tyr Val Phe Ala Val Gly Thr Arg Lys Ala Leu Val Arg Leu  
 260                    265                    270  
 10   Gln Lys Glu Met Gln Asp Leu Ser Glu Phe Cys Ser Asp Lys Pro Lys  
 275                    280                    285  
 Ser Gly Ala Lys Tyr Gly Leu Pro Asp Ser Leu Ala Ile Leu Ser Glu  
 15   290                    295                    300  
 Met Gly Glu Val Thr Asp Gly Met Met Asp Thr Lys Met Val His Phe  
 305                    310                    315                    320  
 20   Leu Thr His Tyr Ala Asp Lys Ile Glu Ser Val His Phe Ser Asp Gln  
 325                    330                    335  
 Phe Ser Gly Pro Lys Ile Met Gln Glu Gly Gln Pro Leu Lys Leu  
 340                    345                    350  
 25   Pro Asp Thr Lys Arg Thr Leu Leu Phe Thr Phe Asn Val Pro Gly Ser  
 355                    360                    365  
 Gly Asn Thr Tyr Pro Lys Asp Met Glu Ala Leu Leu Pro Leu Met Asn  
 30   370                    375                    380  
 Met Val Ile Tyr Ser Ile Asp Lys Ala Lys Lys Phe Arg Leu Asn Arg  
 385                    390                    395                    400  
 35   Glu Gly Lys Gln Lys Ala Asp Lys Asn Arg Ala Arg Val Glu Glu Asn  
 405                    410                    415  
 Phe Leu Lys Leu Thr His Val Gln Arg Gln Glu Ala Ala Gln Ser Arg  
 420                    425                    430  
 40   Arg Glu Glu Lys Lys Arg Ala Glu Lys Glu Arg Ile Met Asn Glu Glu  
 435                    440                    445  
 Asp Pro Glu Lys Gln Arg Arg Leu Glu Glu Ala Ala Leu Arg Arg Glu  
 45   450                    455                    460  
 Gln Lys Lys Leu Glu Lys Lys Gln Met Lys Met Lys Gln Ile Lys Val  
 465                    470                    475                    480  
 50   Lys Ala His Val Lys Pro Ser Gln Arg Phe Glu Phe  
 485                    490

## 55 (2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 36 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

Met Leu Phe Leu Cys Leu Leu Pro Ser Leu Phe Pro Pro Gly Leu Pro  
 1 5 10 15

5 Thr Thr His Tyr Ile Thr Ser Ile Cys Asn Gln Ser Cys Tyr His His  
 20 25 30

Cys Ala Arg Ala  
 10 35

## (2) INFORMATION FOR SEQ ID NO: 73:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 74 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

Met Ala Glu Leu Leu Leu Xaa Val Leu Ser Val Gln Ser Ala Val His  
 1 5 10 15

25 Glu Val Glu Ala Asn Glu Gly Gly Lys Gln Ser His Thr Pro Ala His  
 20 25 30

Arg Gly Trp Asn Arg Arg Ala Ala Glu Val Arg Lys Ala Arg Leu Pro  
 35 40 45

30 Leu Gly Val Thr Val Gly Pro Arg Cys Arg His Ala Val His Pro Ser  
 50 55 60

35 Lys Gly Gly Ile Ser Ala Xaa Ala Val Leu  
 65 70

40 (2) INFORMATION FOR SEQ ID NO: 74:  
 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

Met Gly Ser Ser Gly Leu Leu Ser Leu Leu Val Leu Phe Val Leu Leu  
 1 5 10 15

50 Ala Asn Val Gln Gly Pro Gly Leu Thr Asp Trp Leu Phe Pro Arg Arg  
 20 25 30

Cys Pro Lys Ile Arg Glu Glu Cys Glu Phe Gln Glu Arg Asp Val Cys  
 35 40 45

55 Thr Lys Asp Arg Gln Cys Gln Asp Asn Lys Lys Cys Cys Val Phe Ser  
 50 55 60

60 Cys Gly Lys Lys Cys Leu Asp Leu Lys Gln Asp Val Cys Glu Met Pro  
 65 70 75 80

Lys Glu Thr Gly Pro Cys Leu Ala Tyr Phe Leu His Trp Trp Tyr Asp  
 85 90 95

5 Lys Lys Asp Asn Thr Cys Ser Met Phe Val Tyr Gly Gly Cys Gln Gly  
 100 105 110

Asn Asn Asn Phe Gln Ser Lys Ala Asn Cys Leu Asn Thr Cys Lys  
 115 120 125

10 Asn Lys Arg Phe Pro  
 130

15 (2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 298 amino acids  
 20 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr  
 25 1 5 10 15

Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro  
 20 25 30

30 Lys Asp Gln Gln Val Val Thr Ala Val Xaa Tyr Gln Glu Ala Ile Leu  
 35 40 45

Ala Cys Lys Thr Pro Lys Thr Val Xaa Ser Arg Leu Glu Trp Lys  
 50 55 60

35 Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln  
 65 70 75 80

Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile  
 40 85 90 95

Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser  
 100 105 110

45 Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu  
 115 120 125

Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser  
 130 135 140

50 Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly  
 145 150 155 160

Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu  
 55 165 170 175

Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met  
 180 185 190

60 Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp

	195	200	205
	Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg		
	210	215	220
5	Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile		
	225	230	235
	Ile Ala Ala Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu		
10	245	250	255
	Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser		
	260	265	270
15	Phe Gln Lys Ser Asn Ser Ser Lys Ala Thr Thr Met Ser Glu Asn		
	275	280	285
	Asp Phe Lys His Thr Lys Ser Phe Ile Ile		
20	290	295	

## (2) INFORMATION FOR SEQ ID NO: 76:

25	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 856 amino acids		
	(B) TYPE: amino acid		
	(D) TOPOLOGY: linear		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:		
30	Met Asp Ile Ser Lys Gly Leu Pro Gly Met Gln Gly Gly Leu His Ile		
	1	5	10
	Trp Ile Ser Glu Asn Arg Lys Met Val Pro Val Pro Glu Gly Ala Tyr		
35	20	25	30
	Gly Asn Phe Phe Glu Glu His Cys Tyr Val Ile Leu His Val Pro Gln		
	35	40	45
40	Ser Pro Lys Xaa Thr Gln Gly Ala Ser Ser Asp Leu His Tyr Trp Val		
	50	55	60
	Gly Lys Gln Ala Gly Ala Glu Ala Gln Gly Ala Ala Glu Ala Phe Gln		
45	65	70	75
	Gln Arg Leu Gln Asp Glu Leu Gly Gly Gln Thr Val Leu His Arg Glu		
	85	90	95
50	Ala Gln Gly His Glu Ser Asp Cys Phe Cys Ser Tyr Phe Arg Pro Gly		
	100	105	110
	Ile Ile Tyr Arg Lys Gly Gly Leu Ala Ser Asp Leu Lys His Val Glu		
	115	120	125
55	Thr Asn Leu Phe Asn Ile Gln Arg Leu Leu His Ile Lys Gly Arg Lys		
	130	135	140
	His Val Ser Ala Thr Glu Val Glu Leu Ser Trp Asn Ser Phe Asn Lys		
60	145	150	155

170

Gly Asp Ile Phe Leu Leu Asp Leu Gly Lys Met Met Ile Gln Trp Asn  
 165 170 175

5 Gly Pro Lys Thr Ser Ile Ser Glu Lys Ala Arg Gly Leu Xaa Leu Thr  
 180 185 190

Tyr Ser Leu Arg Asp Arg Glu Arg Gly Gly Arg Ala Gln Ile Gly  
 195 200 205

10 Val Val Asp Asp Glu Ala Lys Ala Pro Asp Leu Met Gln Ile Met Glu  
 210 215 220

Ala Val Leu Gly Arg Arg Val Gly Xaa Leu Arg Ala Ala Thr Pro Ser  
 225 230 235 240

15 Lys Asp Ile Asn Gln Leu Gln Lys Ala Asn Val Arg Leu Tyr His Val  
 245 250 255

Tyr Glu Lys Gly Lys Asp Leu Val Val Leu Glu Leu Ala Thr Pro Pro  
 20 260 265 270

Leu Thr Gln Asp Leu Leu Gln Glu Glu Asp Phe Tyr Ile Leu Asp Gln  
 275 280 285

25 Gly Gly Phe Lys Ile Tyr Val Trp Gln Gly Arg Met Ser Ser Leu Gln  
 290 295 300

Glu Arg Lys Ala Ala Phe Ser Arg Ala Val Gly Phe Ile Gln Ala Lys  
 305 310 315 320

30 Gly Tyr Pro Thr Tyr Thr Asn Val Glu Val Val Asn Asp Gly Ala Glu  
 325 330 335

Ser Ala Ala Phe Lys Gln Leu Phe Arg Thr Trp Ser Glu Lys Arg Arg  
 35 340 345 350

Arg Asn Gln Lys Leu Gly Arg Asp Lys Ser Ile His Val Lys Leu  
 355 360 365

40 Asp Val Gly Lys Leu His Thr Gln Pro Lys Leu Ala Ala Gln Leu Arg  
 370 375 380

Met Val Asp Asp Gly Ser Gly Lys Val Glu Val Trp Cys Ile Gln Asp  
 385 390 395 400

45 Leu His Arg Gln Pro Val Asp Pro Lys Arg His Gly Gln Leu Cys Ala  
 405 410 415

Gly Asn Cys Tyr Leu Val Leu Tyr Thr Tyr Gln Arg Leu Gly Arg Val  
 50 420 425 430

Gln Tyr Ile Leu Tyr Leu Trp Gln Gly His Gln Ala Thr Ala Asp Glu  
 435 440 445

Ile Glu Ala Leu Asn Ser Asn Ala Glu Glu Leu Asp Val Met Tyr Gly  
 55 450 455 460

Gly Val Leu Val Gln Glu His Val Thr Met Gly Ser Glu Pro Pro His  
 465 470 475 480

60

Phe Leu Ala Ile Phe Gln Gly Gln Leu Val Ile Phe Gln Glu Arg Ala  
 485                          490                          495

5    Gly His His Gly Lys Gly Gln Ser Ala Ser Thr Thr Arg Leu Phe Gln  
       500                          505                          510

Val Gln Gly Thr Asp Ser His Asn Thr Arg Thr Met Glu Val Pro Ala  
 515                          520                          525

10   Arg Ala Ser Ser Leu Asn Ser Ser Asp Ile Phe Leu Leu Val Thr Ala  
       530                          535                          540

Ser Val Cys Tyr Leu Trp Phe Gly Lys Gly Cys Asn Gly Asp Gln Arg  
 545                          550                          555                          560

15   Glu Met Ala Arg Val Val Val Thr Val Ile Ser Arg Lys Asn Glu Glu  
       565                          570                          575

Thr Val Leu Glu Gly Gln Glu Pro Pro His Phe Trp Glu Ala Leu Gly  
 20        580                          585                          590

Gly Arg Xaa Pro Tyr Pro Ser Asn Lys Arg Leu Pro Glu Glu Val Pro  
 595                          600                          605

25   Ser Phe Gln Pro Arg Leu Phe Glu Cys Ser Ser His Met Gly Cys Leu  
       610                          615                          620

Val Leu Ala Glu Val Gly Phe Phe Ser Gln Glu Asp Leu Asp Lys Tyr  
 30        625                          630                          635                          640

Asp Ile Met Leu Leu Asp Thr Trp Gln Glu Ile Phe Leu Trp Leu Gly  
       645                          650                          655

Glu Ala Ala Ser Glu Trp Lys Glu Ala Val Ala Trp Gly Gln Glu Tyr  
 35        660                          665                          670

Leu Lys Thr His Pro Ala Gly Arg Ser Pro Xaa Thr Pro Ile Val Leu  
       675                          680                          685

40   Val Lys Gln Gly His Glu Pro Pro Thr Phe Ile Gly Trp Phe Phe Thr  
       690                          695                          700

Trp Asp Pro Tyr Lys Trp Thr Ser His Pro Ser His Lys Glu Val Val  
 45        705                          710                          715                          720

Asp Gly Ser Pro Ala Ala Ala Ser Thr Ile Ser Glu Ile Thr Ala Glu  
       725                          730                          735

Val Asn Asn Phe Arg Leu Ser Arg Trp Pro Gly Asn Gly Arg Ala Gly  
 50        740                          745                          750

Ala Val Ala Leu Gln Ala Leu Lys Gly Ser Gln Asp Ser Ser Glu Asn  
       755                          760                          765

55   Asp Leu Val Arg Ser Pro Lys Ser Ala Gly Ser Arg Thr Ser Ser Ser  
       770                          775                          780

Val Ser Ser Thr Ser Ala Thr Ile Asn Gly Gly Leu Arg Arg Glu Gln  
 60        785                          790                          795                          800

Leu Met His Gln Ala Val Glu Asp Leu Pro Glu Gly Val Asp Pro Ala  
 805 810 815  
 Arg Arg Glu Phe Tyr Leu Ser Asp Ser Asp Phe Gln Asp Ile Phe Gly  
 5 820 825 830  
 Lys Ser Lys Glu Glu Phe Tyr Ser Met Ala Thr Trp Arg Gln Arg Gln  
 835 840 845  
 10 Glu Lys Lys Gln Leu Gly Phe Phe  
 850 855

15 (2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

Met Pro Cys Val Phe Cys Tyr Leu Leu Leu Leu Val Gln Phe Thr Tyr  
 1 5 10 15  
 20 Thr Phe Thr Leu Ser Asn Pro Asn Ser Ser Ser Arg Pro Asp Ser Asp  
 25 20 25 30  
 Phe Asn Phe Leu Lys Ala Ile  
 30 35

35 (2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

Met Ala Leu Ser Val Leu Val Leu Leu Leu Ala Val Leu Tyr Glu  
 1 5 10 15  
 45 Gly Ile Lys Val Gly Lys Ala Ser Cys Ser Thr Arg Tyr Trp  
 20 25 30

50 (2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 45 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Met Pro Ala Leu Val Leu Leu Pro Arg Val Leu Pro Pro Gly Gln Gly  
 1 5 10 15  
 60

Glu Val Gln Arg Val Arg Cys Pro Tyr Val Gly Asn Ser Ser Gly Arg  
 20 25 30  
 Lys Ile Trp Phe Gly Phe Ile Leu Arg Ala Ile Lys His  
 5 35 40 45

- (2) INFORMATION FOR SEQ ID NO: 80:
- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:
- Met Leu Ser Phe Lys Leu Leu Leu Ala Val Ala Leu Gly Phe Phe  
 1 5 10 15
- 20 Glu Gly Asp Ala Lys Phe Gly Glu Arg Asn Glu Gly Ser Gly Gln Gly  
 20 25 30
- Gly Glu Gly Ala  
 35
- 25
- (2) INFORMATION FOR SEQ ID NO: 81:
- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 293 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:
- Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg Leu Ser Arg  
 1 5 10 15
- 40 Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu Ser Ala Ala  
 20 25 30
- Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly Leu Pro Thr  
 35 40 45
- 45 Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg Glu Val Glu  
 50 55 60
- Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn Arg Arg Ser  
 65 70 75 80
- 50 Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe Ser Lys Val  
 85 90 95
- 55 Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met Gly Leu Leu  
 100 105 110
- Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys Pro Pro Leu  
 115 120 125
- 60 Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys Thr Ile Asp

174

	130	135	140
	Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val Glu Phe Phe		
5	145	150	155
	Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile Tyr Ala Asp		
	165	170	175
10	Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly Lys Val Asp		
	180	185	190
	Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val Ser Thr Ser		
	195	200	205
15	Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln Gly Gly Lys		
	210	215	220
	Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg Ala Val Ser		
20	225	230	235
	Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn Leu Asn Glu		
	245	250	255
25	Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp Asn Ile Pro		
	260	265	270
	Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser Asp Gly Glu		
	275	280	285
30	Asn Lys Lys Asp Lys		
	290		

## 35 (2) INFORMATION FOR SEQ ID NO: 82:

	(i) SEQUENCE CHARACTERISTICS:			
	(A) LENGTH: 143 amino acids			
	(B) TYPE: amino acid			
40	(D) TOPOLOGY: linear			
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:			
	Met Arg Gly Leu Gly Leu Trp Leu Leu Gly Ala Met Met Leu Pro Ala			
	1	5	10	15
45	Ile Ala Pro Ser Arg Pro Trp Ala Leu Met Glu Gln Tyr Glu Val Val			
	20	25	30	
50	Leu Pro Trp Arg Leu Pro Gly Pro Arg Val Arg Arg Ala Leu Pro Ser			
	35	40	45	
	His Leu Gly Leu His Pro Glu Arg Val Ser Tyr Val Leu Gly Ala Thr			
	50	55	60	
55	Gly His Asn Phe Thr Leu His Leu Arg Lys Asn Arg Asp Leu Leu Gly			
	65	70	75	80
	Ser Gly Tyr Thr Glu Thr Tyr Thr Ala Ala Asn Gly Ser Glu Val Thr			
	85	90	95	
60				

Glu Gln Pro Arg Gly Gln Asp His Cys Phe Tyr Gln Gly His Leu Glu  
 100 105 110

5 Gly Thr Gly Leu Ser Arg Gln Pro Gln His Leu Cys Arg Pro Gln Gly  
 115 120 125

Phe Leu Pro Gly Gly Val Arg Pro Ala Pro Asp Arg Ala Pro Gly  
 130 135 140

10

(2) INFORMATION FOR SEQ ID NO: 83:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

20 Met Arg Ile Met Leu Leu Phe Thr Ala Ile Leu Ala Phe Ser Leu Ala  
 1 5 10 15

Gln Ser Phe Gly Ala Val Cys Lys Glu Pro Gln Glu Glu Val Val Pro  
 20 25 30

25 Gly Gly Gly Arg Ser Lys Arg Asp Pro Asp Leu Tyr Gln Leu Leu Gln  
 35 40 45

30 Arg Leu Phe Lys Ser His Ser Ser Leu Glu Gly Leu Leu Lys Ala Leu  
 50 55 60

Ser Gln Xaa Ser Thr Asp Pro Lys Glu Ser Thr Ser Pro Glu Lys Arg  
 65 70 75 80

35 Asp Met His Asp Phe Phe Val Gly Xaa Met Gly Lys Arg Ser Val Gln  
 85 90 95

40 Pro Asp Ser Pro Thr Asp Val Asn Gln Glu Asn Val Pro Ser Phe Gly  
 100 105 110

Ile Leu Lys Tyr Pro Pro Arg Ala Glu  
 115 120

45

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

55 Met Val Leu Leu Met Val Trp Val Val Met Ala Val Val Val Glu Ala  
 1 5 10 15

Val Glu Val Thr Met Gly Lys Ala Ala  
 20 25

60

## (2) INFORMATION FOR SEQ ID NO: 85:

5                   (i) SEQUENCE CHARACTERISTICS:  
                       (A) LENGTH: 4 amino acids  
                       (B) TYPE: amino acid  
                       (D) TOPOLOGY: linear  
                      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

10 Ser Leu His Ala  
     1

## 15 (2) INFORMATION FOR SEQ ID NO: 86:

20                   (i) SEQUENCE CHARACTERISTICS:  
                       (A) LENGTH: 235 amino acids  
                       (B) TYPE: amino acid  
                       (D) TOPOLOGY: linear  
                      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Met Pro Trp Val Leu Leu Leu Thr Leu Leu Thr His Ser Ala Val  
     1                5                   10                   15

25                   Ser Val Val Gln Ala Gly Leu Thr Gln Pro Pro Ser Val Ser Lys Asp  
     20               25                   30

30                   Leu Arg Gln Thr Ala Thr Leu Thr Cys Thr Gly Asn Asn Asn Asn Val  
     35               40                   45

                     Gly Asp Gln Gly Ala Ala Trp Leu Gln Gln His Gln Gly His Pro Pro  
     50               55                   60

35                   Lys Leu Leu Ser Tyr Arg Asn Asn Asn Arg Pro Ser Gly Ile Ser Glu  
     65               70                   75                   80

40                   Arg Leu Ser Ala Ser Arg Ser Gly Ala Thr Ser Ser Leu Thr Ile Thr  
     85               90                   95

45                   Gly Leu Gln Pro Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Tyr Asp  
     100             105                   110

50                   Ser Ser Leu Ala Val Trp Met Phe Gly Gly Thr Lys Leu Thr Val  
     115             120                   125

55                   Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser  
     130             135                   140

60                   Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser  
     145             150                   155                   160

                     Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser  
     165             170                   175

65                   Pro Val Lys Ala Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn  
     180             185                   190

70                   Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp  
     195             200                   205

Lys Ser His Lys Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr  
 210                            215                            220

5    Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser  
 225                            230                            235

10 (2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

Met Ser Leu Asn Val Leu Leu Ala Leu Phe Xaa Leu Leu Leu Ala Lys  
 1                            5                                    10                            15

20    Glu Ser Ser Cys Arg Ile Pro Ala Ala Arg Gly Asp Pro Leu Val Leu  
 20                            25                                    30

25    Glu Arg Pro Pro Pro Arg Trp Glu Leu Gln Leu Leu Val Pro Phe Ser  
 35                            40                                    45

Glu Gly Leu Ile Ser Ser Leu Ala Val Ile Met Gly His Ser Leu Phe  
 50                            55                                    60

30    Pro Gly Val Glu Ile Gly Tyr Pro Ala His Lys Phe His Asn Asn Asn  
 65                            70                                    75                            80

35    Thr Ser Arg Lys His Xaa Val  
 85

(2) INFORMATION FOR SEQ ID NO: 88:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

45    Met Ala Leu His Gly Phe His Phe Asp Leu Phe His Phe His Leu Leu  
 1                            5                                    10                            15

50    Leu Phe Gln Leu Leu Xaa Leu Thr Pro Gln Cys Ser Leu Leu Gln Pro  
 20                            25                                    30

Ala Leu Phe Leu Arg Ile Phe Leu Ile His Asp Ser Leu Leu Leu Cys  
 35                            40                                    45

55    Ser Phe Phe Leu Leu Pro Pro Arg Leu Cys Cys Phe Leu Ser Leu His  
 50                            55                                    60

60    Met Cys Gln Phe Gln Glu Val Leu Phe Tyr Ser Gly Thr Val Leu Ile  
 65                            70                                    75                            80

10 (2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

30 (2) INFORMATION FOR SEQ ID NO: 90:

40	Met Glu Val Pro Ala Arg Ala Ser Ser Leu Asn Ser Ser Asp Ile Phe
	1                    5                    10                    15
	Leu Leu Val Thr Ala Ser Val Cys Tyr Leu Trp Phe Gly Lys Gly Leu
	20                    25                    30

	Glu Arg Glu Val Leu Glu Arg Asp Leu Val Leu Pro Leu Leu Cys Lys
	35 40 45
5	Asp Tyr Cys Lys Glu Phe Phe Tyr Thr Cys Arg Gly His Ile Pro Gly
	50 55 60
	Phe Leu Gln Thr Thr Ala Asp Glu Phe Cys Phe Tyr Tyr Ala Arg Lys
	65 70 75 80
10	Asp Gly Gly Leu Cys Phe Pro Asp Phe Pro Arg Lys Gln Val Arg Gly
	85 90 95
	Pro Ala Ser Asn Tyr Leu Asp Gln Met Glu Glu Tyr Asp Lys Val Glu
15	100 105 110
	Glu Ile Ser Arg Lys His Lys His Asn Cys Phe Cys Ile Gln Glu Val
	115 120 125
20	Val Ser Gly Leu Arg Gln Pro Val Gly Ala Leu His Ser Gly Asp Gly
	130 135 140
	Ser Gln Arg Leu Phe Ile Leu Glu Lys Glu Gly Tyr Val Lys Ile Leu
	145 150 155 160
25	Thr Pro Glu Gly Glu Ile Phe Lys Glu Pro Tyr Leu Asp Ile His Lys
	165 170 175
	Leu Val
30	

35	(2) INFORMATION FOR SEQ ID NO: 92:
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 216 amino acids
	(B) TYPE: amino acid
	(D) TOPOLOGY: linear
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:
	Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg Glu Val Glu Ile Leu Met
	1 5 10 15
45	Phe Leu Ser Ala Ile Val Met Met Lys Asn Arg Arg Ser Ile Thr Val
	20 25 30
	Glu Gln His Ile Gly Asn Ile Phe Met Phe Ser Lys Val Ala Asn Thr
	35 40 45
50	Ile Leu Phe Phe Arg Leu Asp Ile Arg Met Gly Leu Leu Tyr Ile Thr
	50 55 60
	Leu Cys Ile Val Phe Leu Met Thr Cys Lys Pro Pro Leu Tyr Met Gly
55	65 70 75 80
	Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys Thr Ile Asp Glu Glu Leu
	85 90 95
60	Glu Arg Asp Lys Arg Val Thr Trp Ile Val Glu Phe Phe Ala Asn Trp

180

	100	105	110
	Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile Tyr Ala Asp Leu Ser Leu		
	115	120	125
5	Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly Lys Val Asp Val Gly Arg		
	130	135	140
10	Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val Ser Thr Ser Pro Leu Thr		
	145	150	155
	Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln Gly Gly Lys Glu Ala Met		
	165	170	175
15	Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg Ala Val Ser Trp Thr Phe		
	180	185	190
	Ser Glu Glu Asn Val Ile Arg Glu Phe Asn Leu Asn Glu Leu Tyr Gln		
20	195	200	205
	Arg Ala Lys Lys Leu Ser Lys Ala		
	210	215	

25

(2) INFORMATION FOR SEQ ID NO: 93:

	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 196 amino acids		
30	(B) TYPE: amino acid		
	(C) TOPOLOGY: linear		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:		
35	Gln Leu Ile Val Thr Ala Arg Thr Thr Arg Gly Leu Asp Pro Leu Phe		
	1	5	10
	15		
	Gly Met Cys Glu Lys Phe Leu Gln Glu Val Asp Phe Phe Gln Arg Tyr		
	20	25	30
40	Phe Ile Ala Asp Leu Pro His Leu Gln Asp Ser Phe Val Asp Lys Leu		
	35	40	45
	Leu Asp Leu Met Pro Arg Leu Met Thr Ser Lys Pro Ala Glu Val Val		
45	50	55	60
	Lys Ile Leu Gln Thr Met Leu Arg Gln Ser Ala Phe Leu His Leu Pro		
	65	70	75
	80		
50	Leu Pro Glu Gln Ile His Lys Ala Ser Ala Thr Ile Ile Glu Pro Ala		
	85	90	95
	Gly Glu Phe Arg Gln Pro Phe Ala Val Tyr Leu Trp Val Gly Gly Cys		
	100	105	110
55	Pro Gly Met Leu Met Gln Pro Trp Ser Met Cys Arg Ile Leu Arg Thr		
	115	120	125
	Leu Leu Arg Ser Arg Val Leu Tyr Pro Asp Gly Gln Xaa Ser Asp Asp		
60	130	135	140

Ser Pro Gln Ala Cys Arg Leu Pro Glu Ser Trp Pro Arg Ala Ala Pro  
 145 150 155 160  
 5 Ala His His Ser Gly Leu Ser Leu Pro His Arg Leu Asp Arg Gly Met  
 165 170 175  
 Pro Gly Gly Ser Glu Ala Ala Ala Gly Leu Gln Leu Gln Cys Ser His  
 180 185 190  
 10 Ser Lys Met Pro  
 195

15 (2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

Ile His Leu Ala Leu Val Glu Leu Leu Lys Asn Leu Thr Lys Tyr Pro  
 1 5 10 15  
 25 Thr Asp Arg Asp Ser Ile Trp Lys Cys Leu Lys Phe Leu Gly Ser Arg  
 20 25 30  
 His Pro Thr Leu Val Leu Pro Leu Val Pro Glu Leu Leu Ser Thr His  
 30 35 40 45  
 Pro Phe Phe Asp Thr Ala Glu Pro Asp Met Asp Asp Pro Ala Tyr Ile  
 50 55 60  
 35 Ala Val Leu Val Leu Ile Phe Asn Ala Ala Lys Thr Cys Pro Thr Met  
 65 70 75 80  
 Pro Ala Leu Phe Ser Asp His Thr Phe Arg His Tyr Ala Tyr Leu Arg  
 85 90 95  
 40 Asp Ser Leu Ser His Leu Val Pro Ala Leu Arg Leu Pro Gly Arg Lys  
 100 105 110  
 45 Leu Val Ser Ser Ala Val Ser Pro Ser Ile Ile Pro Gln Glu Asp Pro  
 115 120 125  
 Ser Gln Gln Phe Leu Gln Gln Ser Leu Glu Arg Val Tyr Ser Leu Gln  
 130 135 140  
 50 His Leu Asp Pro Gln Gly Ala Gln Glu Leu Leu Glu Phe Thr Ile Arg  
 145 150 155 160  
 Asp Leu Gln Arg Leu Gly Glu Leu Gln Ser Glu Leu Ala Gly Val Ala  
 165 170 175  
 55 Asp Phe Ser Ala Thr Tyr Leu Arg Cys Gln Leu Leu Leu Ile Lys Ala  
 180 185 190  
 60 Leu Gln Glu Lys Leu Trp Asn Val Ala Ala Pro Leu Tyr Leu Lys Gln  
 195 200 205

Ser Asp Leu Ala Ser Ala Ala Ala Lys Gln Ile Met Glu Glu Thr Tyr  
 210                    215                    220

5    Lys Met Glu Phe Met Tyr Ser Gly Val Glu Asn Lys Gln Val Val Ile  
 225                    230                    235                    240

Ile His His Met Arg Leu Gln Ala Lys Ala Leu Gln Leu Ile Val  
 245                    250                    255

10

## (2) INFORMATION FOR SEQ ID NO: 95:

15                    (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 137 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

20                    Arg Phe Tyr Ser Asn Ser Cys Cys Leu Cys Cys His Val Arg Thr Gly  
 1                    5                        10                        15

25                    Thr Ile Leu Leu Gly Val Trp Tyr Leu Ile Ile Asn Ala Val Val Leu  
 20                    25                        30

Leu Ile Leu Ser Ala Leu Ala Asp Pro Asp Gln Tyr Asn Phe Ser  
 35                    40                        45

30                    Ser Ser Glu Leu Gly Gly Asp Phe Glu Phe Met Asp Asp Ala Asn Met  
 50                    55                        60

Cys Ile Ala Ile Ala Ile Ser Leu Leu Met Ile Leu Ile Cys Ala Met  
 65                    70                        75                        80

35                    Ala Thr Tyr Gly Ala Tyr Lys Gln Arg Ala Ala Gly Ile Ile Pro Phe  
 85                    90                        95

40                    Phe Cys Tyr Gln Ile Phe Asp Phe Ala Leu Asn Met Leu Val Ala Ile  
 100                   105                        110

Thr Val Leu Ile Tyr Pro Asn Ser Ile Gln Glu Tyr Ile Arg Gln Leu  
 115                   120                        125

45                    Pro Pro Asn Phe Pro Tyr Arg Asp Asp  
 130                   135

## 50                    (2) INFORMATION FOR SEQ ID NO: 96:

55                    (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 87 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

Phe Pro Thr Glu Met Met Ser Cys Ala Val Asn Pro Thr Cys Leu Val  
 1                    5                        10                        15

60

Leu Ile Ile Leu Leu Phe Ile Ser Ile Ile Leu Thr Phe Lys Gly Tyr  
 20 25 30

5 Leu Ile Ser Cys Val Trp Asn Cys Tyr Arg Tyr Ile Asn Gly Arg Asn  
 35 40 45

Ser Ser Asp Val Leu Val Tyr Val Thr Ser Asn Asp Thr Thr Val Leu  
 50 55 60

10 Leu Pro Pro Tyr Asp Asp Ala Thr Val Asn Gly Ala Ala Lys Glu Pro  
 65 70 75 80

Pro Pro Pro Tyr Val Ser Ala  
 85

15

## (2) INFORMATION FOR SEQ ID NO: 97:

20 (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 97 amino acids  
     (B) TYPE: amino acid  
     (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

25 Ile Ala Pro Ser Arg Pro Trp Ala Leu Met Glu Gln Tyr Glu Val Val  
 1 5 10 15

30 Leu Pro Trp Arg Leu Pro Gly Pro Arg Val Arg Arg Ala Leu Pro Ser  
 20 25 30

His Leu Gly Leu His Pro Glu Arg Val Ser Tyr Val Leu Gly Ala Thr  
 35 40 45

35 Gly His Asn Phe Thr Leu His Leu Arg Lys Asn Arg Asp Leu Leu Gly  
 50 55 60

Ser Gly Tyr Thr Glu Thr Tyr Thr Ala Ala Asn Gly Ser Glu Val Thr  
 65 70 75 80

40 Glu Gln Pro Arg Gly Gln Asp His Cys Phe Tyr Gln Gly His Leu Glu  
 85 90 95

45 Gly

## (2) INFORMATION FOR SEQ ID NO: 98:

50 (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 240 amino acids  
     (B) TYPE: amino acid  
     (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

55 Pro Asp Ser Ala Ala Ser Leu Ser Thr Cys Ala Gly Leu Arg Gly Phe  
 1 5 10 15

60 Phe Gln Val Gly Ser Asp Leu His Leu Ile Glu Pro Leu Asp Glu Gly  
 20 25 30

Gly Glu Gly Gly Arg His Ala Val Tyr Gln Ala Glu His Leu Leu Gln  
 35 40 45

5 Thr Ala Gly Thr Cys Gly Val Ser Asp Asp Ser Leu Gly Ser Leu Leu  
 50 55 60

Gly Pro Arg Thr Ala Ala Val Phe Arg Pro Arg Pro Gly Asp Ser Leu  
 65 70 75 80

10 Pro Ser Arg Glu Thr Arg Tyr Val Glu Leu Tyr Val Val Val Asp Asn  
 85 90 95

Ala Glu Phe Gln Met Leu Gly Ser Glu Ala Ala Val Arg His Arg Val  
 15 100 105 110

Leu Glu Val Val Asn His Val Asp Lys Leu Tyr Gln Lys Leu Asn Phe  
 115 120 125

20 Arg Val Val Leu Val Gly Leu Glu Ile Trp Asn Ser Gln Asp Arg Phe  
 130 135 140

His Val Ser Pro Asp Pro Ser Val Thr Leu Glu Asn Leu Leu Thr Trp  
 145 150 155 160

25 Gln Ala Arg Gln Arg Thr Arg Arg His Leu His Asp Asn Val Gln Leu  
 165 170 175

Ile Thr Gly Val Asp Phe Thr Gly Thr Thr Val Gly Phe Ala Arg Val  
 30 180 185 190

Ser Ala Met Cys Ser His Ser Ser Gly Ala Val Asn Gln Asp His Ser  
 195 200 205

35 Lys Asn Pro Val Gly Val Ala Cys Thr Met Ala His Glu Met Gly His  
 210 215 220

Asn Leu Gly Met Asp His Asp Glu Asn Val Gln Gly Cys Arg Cys Gln  
 225 230 235 240

40

(2) INFORMATION FOR SEQ ID NO: 99:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 118 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

Phe Glu Ala Gly Arg Cys Ile Met Ala Arg Pro Ala Leu Ala Pro Ser  
 1 5 10 15

55 Phe Pro Arg Met Phe Ser Asp Cys Ser Gln Ala Tyr Leu Glu Ser Phe  
 20 25 30

Leu Glu Arg Pro Gln Ser Val Cys Leu Ala Asn Ala Pro Asp Leu Ser  
 35 40 45

60

185

	His	Leu	Val	Gly	Gly	Pro	Val	Cys	Gly	Asn	Leu	Phe	Val	Glu	Arg	Gly
	50					55				60						
5	Glu	Gln	Cys	Asp	Cys	Gly	Pro	Pro	Glu	Asp	Cys	Arg	Asn	Arg	Cys	Cys
	65					70			75				80			
	Asn	Ser	Thr	Thr	Cys	Gln	Leu	Ala	Glu	Gly	Ala	Gln	Cys	Ala	His	Gly
						85			90				95			
10	Thr	Cys	Cys	Gln	Glu	Cys	Lys	Val	Lys	Pro	Ala	Gly	Glu	Leu	Cys	Arg
							100		105				110			
	Pro	Lys	Lys	Asp	Met	Cys										
15						115										

## (2) INFORMATION FOR SEQ ID NO: 100:

20	(i)	SEQUENCE CHARACTERISTICS:														
		(A)	LENGTH:	330	amino acids											
		(B)	TYPE:	amino acid												
		(D)	TOPOLOGY:	linear												
25	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 100:														
	Met	Leu	Pro	Asp	Trp	Lys	Xaa	Ser	Leu	Ile	Leu	Met	Ala	Tyr	Ile	Ile
	1								10			15				
30	Ile	Phe	Leu	Thr	Gly	Leu	Pro	Ala	Asn	Leu	Ala	Leu	Arg	Ala	Phe	
						20			25			30				
	Val	Gly	Arg	Ile	Arg	Gln	Pro	Gln	Pro	Ala	Pro	Val	His	Ile	Leu	Leu
						35			40			45				
35	Leu	Ser	Leu	Thr	Leu	Ala	Asp	Leu	Pro	Phe						
						50			55			60				
	Lys	Ile	Ile	Glu	Ala	Ala	Ser	Asn	Phe	Arg	Trp	Tyr	Leu	Pro	Lys	Val
						65			70			75			80	
40	Val	Cys	Ala	Leu	Thr	Ser	Phe	Gly	Phe	Tyr	Ser	Ser	Ile	Tyr	Cys	Ser
						85			90			95				
45	Thr	Trp	Leu	Leu	Ala	Gly	Ile	Ser	Ile	Glu	Arg	Tyr	Leu	Gly	Val	Ala
						100			105			110				
	Phe	Pro	Val	Gln	Tyr	Lys	Leu	Ser	Arg	Arg	Pro	Leu	Tyr	Gly	Val	Ile
						115			120			125				
50	Ala	Ala	Leu	Val	Ala	Trp	Val	Met	Ser	Phe	Gly	His	Cys	Thr	Ile	Val
						130			135			140				
	Ile	Ile	Xaa	Gln	Tyr	Leu	Asn	Thr	Thr	Glu	Gln	Val	Arg	Ser	Gly	Asn
						145			150			155			160	
55	Glu	Ile	Thr	Cys	Tyr	Glu	Asn	Phe	Thr	Asp	Asn	Gln	Leu	Asp	Val	Val
						165			170			175				
60	Leu	Pro	Val	Arg	Xaa	Glu	Leu	Cys	Leu	Val	Leu	Phe	Phe	Xaa	Pro	Met
						180			185			190				

Ala Val Thr Ile Phe Cys Tyr Trp Arg Phe Val Trp Ile Met Leu Ser  
 195 200 205

5 Gln Pro Leu Val Gly Ala Gln Arg Arg Arg Arg Ala Val Gly Leu Ala  
 210 215 220

Val Val Thr Leu Leu Asn Phe Leu Val Cys Phe Gly Pro Tyr Asn Val  
 225 230 235 240

10 Ser His Leu Val Gly Tyr His Gln Arg Lys Ser Pro Trp Trp Arg Ser  
 245 250 255

Ile Ala Val Xaa Phe Ser Ser Leu Asn Ala Ser Leu Asp Pro Leu Leu  
 15 260 265 270

Phe Tyr Phe Ser Ser Ser Val Val Arg Arg Ala Phe Gly Arg Gly Leu  
 275 280 285

20 Gln Val Leu Arg Asn Gln Gly Ser Ser Leu Leu Gly Arg Arg Gly Lys  
 290 295 300

Asp Thr Ala Glu Gly Thr Asn Glu Asp Arg Gly Val Gly Gln Gly Glu  
 305 310 315 320

25 Gly Met Pro Ser Ser Asp Phe Thr Thr Glu  
 325 330

30 (2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 17 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

Cys Ser Thr Trp Leu Leu Ala Gly Ile Ser Ile Glu Arg Tyr Leu Gly  
 40 1 5 10 15

Val

45 (2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:  
 50 (A) LENGTH: 94 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

Cys Thr Ile Val Ile Ile Xaa Gln Tyr Leu Asn Thr Thr Glu Gln Val  
 55 1 5 10 15

Arg Ser Gly Asn Glu Ile Thr Cys Tyr Glu Asn Phe Thr Asp Asn Gln  
 20 25 30

60

Leu Asp Val Val Leu Pro Val Arg Xaa Glu Leu Cys Leu Val Leu Phe  
                  35                        40                         45  
 Phe Xaa Pro Met Ala Val Thr Ile Phe Cys Tyr Trp Arg Phe Val Trp  
      5            50                    55                    60  
 Ile Met Leu Ser Gln Pro Leu Val Gly Ala Gln Arg Arg Arg Arg Ala  
      65                    70                    75                    80  
 10 Val Gly Leu Ala Val Val Thr Leu Leu Asn Phe Leu Val Cys  
      85                    90

15 (2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 143 amino acids  
     (B) TYPE: amino acid  
     (D) TOPOLOGY: linear  
 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:  
  
 Gly Leu Pro Ala Ala Arg Val Arg Trp Glu Ser Ser Phe Ser Arg Thr  
      1                    5                    10                    15  
 25 Val Val Ala Pro Ser Ala Val Ala Xaa Lys Arg Pro Pro Glu Pro Thr  
      20                    25                    30  
  
 30 Thr Pro Trp Gln Glu Asp Pro Glu Pro Asp Glu Asn Leu Tyr Glu  
      35                    40                    45  
  
 Lys Asn Pro Asp Ser His Gly Tyr Asp Lys Asp Pro Val Leu Asp Val  
      50                    55                    60  
  
 35 Trp Asn Met Arg Leu Val Phe Phe Gly Val Ser Ile Ile Leu Val  
      65                    70                    75                    80  
  
 40 Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro Asp Tyr Arg Cys Thr Gly  
      85                    90                    95  
  
 45 Cys Pro Arg Ala Trp Asp Gly Met Lys Glu Trp Ser Arg Arg Glu Ala  
      100                    105                    110  
  
 50 Glu Arg Leu Val Lys Tyr Arg Glu Ala Asn Gly Leu Pro Ile Met Glu  
      115                    120                    125  
  
 Ser Asn Cys Phe Asp Pro Ser Lys Ile Gln Leu Pro Glu Asp Glu  
      130                    135                    140

50

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 36 amino acids  
     (B) TYPE: amino acid  
     (D) TOPOLOGY: linear  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:  
  
 60 Pro Glu Lys Arg Asp Met His Asp Phe Phe Val Gly Leu Met Gly Lys

1                   5                   10                   15  
Arg Ser Val Gln Pro Asp Ser Pro Thr Asp Val Asn Gln Glu Asn Val  
20                   25                   30  
5                   Pro Ser Phe Gly  
35

10

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
15                   (B) TYPE: amino acid  
                     (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

Lys Arg Asp Met His Asp Phe Phe Val Gly Leu Met Gly Lys Arg  
20                   1                   5                   10                   15

25

(2) INFORMATION FOR SEQ ID NO: 106:

- 25                   (i) SEQUENCE CHARACTERISTICS:  
                     (A) LENGTH: 10 amino acids  
                     (B) TYPE: amino acid  
                     (D) TOPOLOGY: linear  
30                   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

Asp Met His Asp Phe Phe Val Gly Leu Met  
1                   5                   10

35

(2) INFORMATION FOR SEQ ID NO: 107:

- 40                   (i) SEQUENCE CHARACTERISTICS:  
                     (A) LENGTH: 16 amino acids  
                     (B) TYPE: amino acid  
                     (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

45                   Glu Trp Glu Ala Thr Glu Glu Met Glu Trp Ile Ile Arg Glu Ala Met  
                     1                   5                   10                   15

50

(2) INFORMATION FOR SEQ ID NO: 108:

- 55                   (i) SEQUENCE CHARACTERISTICS:  
                     (A) LENGTH: 35 amino acids  
                     (B) TYPE: amino acid  
                     (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

60                   Trp Glu Trp Gly Thr Ile Thr Val Glu Asp Met Val Leu Leu Met Val  
                     1                   5                   10                   15

Trp Val Val Met Ala Val Val Val Glu Ala Val Glu Val Thr Met Gly  
20 25 30

5 Lys Ala Ala  
35

10 (2) INFORMATION FOR SEQ ID NO: 109:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
15 (D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

Gly Met Gly Gly Tyr Gly Arg Asp Gly Met Asp Asn Gln Gly Gly Tyr  
1 5 10 15  
20 Gly Ser

25 (2) INFORMATION FOR SEQ ID NO: 110:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 43 amino acids  
30 (B) TYPE: amino acid  
(C) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

Gly Met Gly Asn Asn Tyr Ser Gly Gly Tyr Gly Thr Pro Asp Gly Leu  
35 1 5 10 15  
Gly Gly Tyr Gly Arg Gly Gly Ser Gly Gly Tyr Tyr Gly Gln  
20 25 30  
40 Gly Gly Met Ser Gly Gly Trp Arg Gly Met  
35 40

45 (2) INFORMATION FOR SEQ ID NO: 111:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
50 (B) TYPE: amino acid  
(C) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

Phe Thr His Ser Phe Ile Leu Glu His Ala Phe Ser Leu Leu Ile Thr  
55 1 5 10 15  
Leu Pro Val Ser Ser Trp Ala Ala Asn Asn  
20 25

(2) INFORMATION FOR SEQ ID NO: 112:

5                   (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:  
  
 10 Cys Glu Met Pro Lys Glu Thr Gly Pro Cys Leu Ala Tyr Phe Leu His  
       1                   5                   10                   15  
  
 15 Trp Trp Tyr Asp Lys Lys Asp Asn Thr Cys Ser Met Phe Val Tyr Gly  
       20                   25                   30  
  
 20 Gly Cys Gln Gly Asn Asn Asn Phe Gln Ser Lys Ala Asn Cys Leu  
       35                   40                   45  
  
 25 Asn Thr Cys  
       50

(2) INFORMATION FOR SEQ ID NO: 113:

Val Asn Asp Gly Ala Glu Ser Ala Ala Phe Lys Gln Leu Phe Arg Thr  
165 170 175

5 Trp Ser Glu Lys Arg Arg Arg Asn Gln Lys Xaa Gly Gly Arg Asp Lys  
180 185 190

Ser Ile His Val Lys Leu Asp Val Gly Lys Leu His Thr Gln Pro Lys  
195 200 205

10 Leu Ala Ala Gln Leu Arg Met Val Asp Asp Gly Ser Gly Lys Val Glu  
210 215 220

15 Val Trp Cys Ile Gln Asp Leu His Arg Gln Pro Val Asp Pro Lys Arg  
225 230 235 240

His Gly Gln Leu Cys Ala Gly Asn Cys Tyr Leu Val Leu Tyr Thr Tyr  
245 250 255

20 Gln Arg Leu Gly Arg Val Gln Tyr Ile Leu Tyr Leu Trp Gln Gly His  
260 265 270

Gln Ala Thr Ala Asp Glu Ile Glu Ala Leu Asn Ser Asn Ala Glu Glu  
275 280 285

25 Leu Asp Val Met Tyr Gly Gly Val Leu Val Gln Glu His Val Thr Met  
290 295 300

30 Gly Ser Glu Pro Pro His Phe Leu Ala Ile Phe Gln Gly Gln Leu Val  
305 310 315 320

Ile Phe Gln Glu Arg Ala Gly His His Gly Lys Gly Gln Ser Ala Ser  
325 330 335

35 Thr Thr Arg Leu Phe Gln Val Gln Gly Thr Asp Ser His Asn Thr Arg  
340 345 350

Thr Met Glu Val Pro Ala Arg Ala Ser Ser Leu Asn Ser Ser Asp Ile  
355 360 365

40 Phe Leu Leu Val Thr Ala Ser Val Cys Tyr Leu Trp Phe Gly Lys Gly  
370 375 380

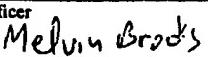
**INDICATIONS RELATING TO A DEPOSITED MICROORGANISM**

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>30</u> , line <u>N/A</u>			
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>			
Name of depositary institution      American Type Culture Collection			
Address of depositary institution ( <i>including postal code and country</i> )  12301 Parklawn Drive Rockville, Maryland 20852 United States of America			
Date of deposit      March 7, 1997	Accession Number      97921		
<b>C. ADDITIONAL INDICATIONS</b> ( <i>leave blank if not applicable</i> )      This information is continued on an additional sheet <input type="checkbox"/>			
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> ( <i>if the indications are not for all designated States</i> )			
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> ( <i>leave blank if not applicable</i> )  The indications listed below will be submitted to the International Bureau later ( <i>specify the general nature of the indications, e.g., "Accession Number of Deposit"</i> )			
<p>For receiving Office use only</p> <p><input checked="" type="checkbox"/> This sheet was received with the international application</p> <p>Authorized officer <i>Melvin Brooks (703) 305-5163</i></p>		<p>For International Bureau use only</p> <p><input type="checkbox"/> This sheet was received by the International Bureau on:</p> <p>Authorized officer</p>	

**INDICATIONS RELATING TO A DEPOSITED MICROORGANISM**

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>31</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b>	
Name of depositary institution      American Type Culture Collection	
Address of depositary institution ( <i>including postal code and country</i> ) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit    March 7, 1997	Accession Number    97922
<b>C. ADDITIONAL INDICATIONS</b> ( <i>leave blank if not applicable</i> )    This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> ( <i>if the indications are not for all designated States</i> )	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> ( <i>leave blank if not applicable</i> ) The indications listed below will be submitted to the International Bureau later ( <i>specify the general nature of the indications, e.g., "Accession Number of Deposit"</i> )	
For receiving Office use only	
<input checked="" type="checkbox"/> This sheet was received with the international application  Authorized officer  (703) 305-5163	
For International Bureau use only	
<input type="checkbox"/> This sheet was received by the International Bureau on:  Authorized officer	

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<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution ( <i>including postal code and country</i> ) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 22, 1997	Accession Number 209070
<b>C. ADDITIONAL INDICATIONS</b> ( <i>leave blank if not applicable</i> ) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> ( <i>if the indications are not for all designated States</i> )	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> ( <i>leave blank if not applicable</i> ) The indications listed below will be submitted to the International Bureau later ( <i>specify the general nature of the indications, e.g., "Accession Number of Deposit"</i> )	
For receiving Office use only	
<input checked="" type="checkbox"/> This sheet was received with the international application	For International Bureau use only
Authorized officer <i>Melvin Brooks (703)355-5163</i>	Authorized officer

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<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution ( <i>including postal code and country</i> ) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit    May 29, 1997	Accession Number    209083
<b>C. ADDITIONAL INDICATIONS</b> ( <i>leave blank if not applicable</i> )    This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> ( <i>if the indications are not for all designated States</i> )	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> ( <i>leave blank if not applicable</i> ) The indications listed below will be submitted to the International Bureau later ( <i>specify the general nature of the indications, e.g., "Accession Number of Deposit"</i> )	
For receiving Office use only	
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Authorized officer	

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Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution ( <i>including postal code and country</i> ) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit    December 12, 1997	Accession Number    209551
<b>C. ADDITIONAL INDICATIONS</b> ( <i>leave blank if not applicable</i> )    This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> ( <i>if the indications are not for all designated States</i> )	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> ( <i>leave blank if not applicable</i> ) The indications listed below will be submitted to the International Bureau later ( <i>specify the general nature of the indications, e.g., "Accession Number of Deposit"</i> )	
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Authorized officer <i>Melvin Brooks (303) 355-5163</i>	Authorized officer

**What Is Claimed Is:**

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group consisting of:
  - (a) a polynucleotide fragment of SEQ ID NO:X or a polynucleotide fragment of the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
  - (b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:Y or a polypeptide fragment encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
  - (c) a polynucleotide encoding a polypeptide domain of SEQ ID NO:Y or a polypeptide domain encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
  - (d) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:Y or a polypeptide epitope encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
  - (e) a polynucleotide encoding a polypeptide of SEQ ID NO:Y or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X,
- 10 20 having biological activity;
  - (f) a polynucleotide which is a variant of SEQ ID NO:X;
  - (g) a polynucleotide which is an allelic variant of SEQ ID NO:X;
  - (h) a polynucleotide which encodes a species homologue of the SEQ ID NO:Y;
  - (i) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(h), wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A residues or of only T residues.
- 25 30 35 2. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding a secreted protein.
  3. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding the sequence identified as SEQ ID NO:Y or the polypeptide encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

4. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises the entire nucleotide sequence of SEQ ID NO:X or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

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5. The isolated nucleic acid molecule of claim 2, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

10

6. The isolated nucleic acid molecule of claim 3, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

15

7. A recombinant vector comprising the isolated nucleic acid molecule of claim 1.

8. A method of making a recombinant host cell comprising the isolated nucleic acid molecule of claim 1.

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9. A recombinant host cell produced by the method of claim 8.

10. The recombinant host cell of claim 9 comprising vector sequences.

25

11. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of:

(a) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(b) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z, having biological activity;

30

(c) a polypeptide domain of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(d) a polypeptide epitope of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

35

(e) a secreted form of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(f) a full length protein of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

- (g) a variant of SEQ ID NO:Y;
- (h) an allelic variant of SEQ ID NO:Y; or
- (i) a species homologue of the SEQ ID NO:Y.

12. The isolated polypeptide of claim 11, wherein the secreted form or the  
5 full length protein comprises sequential amino acid deletions from either the C-terminus  
or the N-terminus.

13. An isolated antibody that binds specifically to the isolated polypeptide of  
claim 11.

10 14. A recombinant host cell that expresses the isolated polypeptide of claim  
11.

15 15. A method of making an isolated polypeptide comprising:  
(a) culturing the recombinant host cell of claim 14 under conditions such that  
said polypeptide is expressed; and  
(b) recovering said polypeptide.

20 16. The polypeptide produced by claim 15.

17. A method for preventing, treating, or ameliorating a medical condition,  
comprising administering to a mammalian subject a therapeutically effective amount of  
the polypeptide of claim 11 or the polynucleotide of claim 1.

25 18. A method of diagnosing a pathological condition or a susceptibility to a  
pathological condition in a subject comprising:  
(a) determining the presence or absence of a mutation in the polynucleotide of  
claim 1; and  
(b) diagnosing a pathological condition or a susceptibility to a pathological  
30 condition based on the presence or absence of said mutation.

19. A method of diagnosing a pathological condition or a susceptibility to a  
pathological condition in a subject comprising:  
(a) determining the presence or amount of expression of the polypeptide of  
35 claim 11 in a biological sample; and  
(b) diagnosing a pathological condition or a susceptibility to a pathological  
condition based on the presence or amount of expression of the polypeptide.

20. A method for identifying a binding partner to the polypeptide of claim 11 comprising:

- 5           (a) contacting the polypeptide of claim 11 with a binding partner; and  
             (b) determining whether the binding partner effects an activity of the polypeptide.

21. The gene corresponding to the cDNA sequence of SEQ ID NO:Y.

10          22. A method of identifying an activity in a biological assay, wherein the method comprises:

- 15           (a) expressing SEQ ID NO:X in a cell;  
             (b) isolating the supernatant;  
             (c) detecting an activity in a biological assay; and  
             (d) identifying the protein in the supernatant having the activity.

23. The product produced by the method of claim 22.